



SEQUENCE LISTING

#9

RECEIVED

AUG 27 2001

TECH CENTER 1600/2900

<110> Shimkets et al

<120> Novel polynucleotides and polypeptides encoded thereby

<130> 15966-552

<140> 09/584,411

<141> 2000-05-31

<150> USSN 60/137,322

<151> 1999-06-03

<150> USSN 60/189,810

<151> 2000-03-16

<150> USSN 60/191,158

<151> 2000-03-22

<150> USSN 60/193,086

<151> 2000-03-30

<150> USSN 60/201,388

<151> 2000-05-03

<160> 93

<170> PatentIn Ver. 2.0

<210> 1

<211> 836

<212> DNA

<213> Artificial Sequence

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<221> CDS

<222> (189)..(695)

<220>

<223> Description of Artificial Sequence: chemically
synthesized

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gcggccgccca cctggagttt cttcagactc cagatttccc tgtcaaccac gaggagtcca 120

gagaggaaac gcggagcgga gacaacagta cctgacgcct ctttcagccc gggatcgccc 180

cagcaggg atg ggc gac aag atc tgg ctg ccc ttc ccc gtg ctc ctt ctg 230

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu

1

5

10

gcc gct ctg ctt cgg gtg ctg ctg cct ggg gcg gcc ggc ttc aca cct 278

Ala Ala Leu Leu Arg Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro

15

20

25

30

tcc ctc gat agc gac ttc acc ttt acc ctt ccc gcc ggc cag aag gag 326

Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu

35

40

45

tgc ttc tac cag ccc atg ccc ctg aag gcc tcg ctg gag atc gag tac 374

Cys Phe Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr

50

55

60

caa gtt tta gat gga gca gga tta gat att gat ttc cat ctt acc tct 422

Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Thr Ser

65

70

75

cca gaa ggc aaa acc tta gtt ttt gaa caa aga aaa tca gat gga gtt 470

Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val

80

85

90

cac act gta gag act gaa gtt ggt gat tac atg ttc tgc ttt gac aat 518

His Thr Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn

95 100 105 110

aca ttc agc acc att tct gag aag gtg att ttc ttt gaa tta atc ctg 566

Thr Phe Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu

115 120 125

gat aat atg gga gaa cag gca caa gaa caa gaa gat tgg aag aaa tat 614

Asp Asn Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr

130 135 140

att act ggc aca gat ata ttg gat atg aaa ctg gaa gac atc ctg gac 662

Ile Thr Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Asp

145 150 155

ctg ccc ggg cgg ccg ctc gag ccc tat agt gag taagtctgga ggcccgggcg 715

Leu Pro Gly Arg Pro Leu Glu Pro Tyr Ser Glu

160 165

gccgctcctg cagtagggta ccgagctcgt cgacgcatgc tgatctagat ctttaattaac 775

acgtggtgcc aagctttgga agactcagct tttgttcctt ttagtgaggg ttaatttcga 835

<210> 2

<211> 169

<212> PRT

<213> Artificial Sequence

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<221> variant

<222> (1)..(169)

<223> where Xaa can any amino acid

<400> 2

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala

1 5 10 15

Leu Leu Arg Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu

20 25 30

Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe

35 40 45

Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val

50	55	60	
Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Thr Ser Pro Glu			
65	70	75	80
Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr			
	85	90	95
Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe			
	100	105	110
Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn			
	115	120	125
Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr			
	130	135	140
Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Asp Leu Pro			
145	150	155	160
Gly Arg Pro Leu Glu Pro Tyr Ser Glu			
	165		

<210> 3

<211> 2342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (110)..(1750)

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<221> variation

<222> (1)..(711)

<223> where n can be any nucleotide

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cgacagactg aaggacagcg gcaccgccag acggccagaa agttccgcc atg agc tgg 118

Met Ser Trp

1

ggc acg gag ctg tgg gat cag ttc gac agc tta gac aag cat aca caa 166

Gly Thr Glu Leu Trp Asp Gln Phe Asp Ser Leu Asp Lys His Thr Gln

5

10

15

tgg gga att gac ttc ttg gaa aga tat gcc aaa ttt gtt aaa gag agg 214

Trp Gly Ile Asp Phe Leu Glu Arg Tyr Ala Lys Phe Val Lys Glu Arg

20 25 30 35

ata gaa att gaa cag aac tat gcg aaa caa ttg aga aat ctg gtt aag 262

Ile Glu Ile Glu Gln Asn Tyr Ala Lys Gln Leu Arg Asn Leu Val Lys

40 45 50

aag tac tgc ccc aaa cgt tca tcc aaa gat gaa gag cca cgg ttt acc 310

Lys Tyr Cys Pro Lys Arg Ser Ser Lys Asp Glu Glu Pro Arg Phe Thr

55 60 65

tcg tgt gta gcc ttt ttt aat atc ctt aat gag tta aat gac tat gca 358

Ser Cys Val Ala Phe Phe Asn Ile Leu Asn Glu Leu Asn Asp Tyr Ala

70 75 80

gga cag cga gaa gtt gta gca gaa gaa atg gcg cac aga gtg tat ggt 406

Gly Gln Arg Glu Val Val Ala Glu Glu Met Ala His Arg Val Tyr Gly

85 90 95

gaa tta atg aga cat gct cat gat ctg aaa act gaa aga aaa atg cat 454

Glu Leu Met Arg His Ala His Asp Leu Lys Thr Glu Arg Lys Met His

100 105 110 115

ctg caa gaa ggc cga aaa gct cac caa tct ctt gcc atg tgc tgg aac 502

Leu Gln Glu Gly Arg Lys Ala His Gln Ser Leu Ala Met Cys Trp Asn

120

125

130

cag atg gat aat agt aaa aag aag ttt gaa aga gaa tgt aga gag gca 550

Gln Met Asp Asn Ser Lys Lys Lys Phe Glu Arg Glu Cys Arg Glu Ala

135

140

145

gaa aag gcc cac cag agt tat gaa aga ttg gat aat gat act aat gca 598

Glu Lys Ala His Gln Ser Tyr Glu Arg Leu Asp Asn Asp Thr Asn Ala

150

155

160

acc aag gca gat gtt gaa aat gcc aaa cag cag ttg aat ctg cgt acg 646

Thr Lys Ala Asp Val Glu Asn Ala Lys Gln Gln Leu Asn Leu Arg Thr

165

170

175

cat atg gcc gat gaa aat aaa aat gca tat gct gca caa tta caa aac 694

His Met Ala Asp Glu Asn Lys Asn Ala Tyr Ala Ala Gln Leu Gln Asn

180

185

190

195

ttt aat gga gaa caa cat aaa cat ttt tat gta gtg att cct cag att 742

Phe Asn Gly Glu Gln His Lys His Phe Tyr Val Val Ile Pro Gln Ile

200

205

210

tac aag caa cta caa gaa atg gac gaa cga agg act att aaa ctc agt 790

Tyr Lys Gln Leu Gln Glu Met Asp Glu Arg Arg Thr Ile Lys Leu Ser

215

220

225

gag tgt tac aga gga ttt gct gac tca gaa cgc aaa gtt att ccc atc 838

Glu Cys Tyr Arg Gly Phe Ala Asp Ser Glu Arg Lys Val Ile Pro Ile

230

235

240

att tca aaa tgt ttg gaa gga atg att ctt gca gca aaa tca gtt gat 886

Ile Ser Lys Cys Leu Glu Gly Met Ile Leu Ala Ala Lys Ser Val Asp

245

250

255

gaa aga aga gac tct caa atg gtg gta gac tcc ttc aaa tct ggt ttt 934

Glu Arg Arg Asp Ser Gln Met Val Val Asp Ser Phe Lys Ser Gly Phe

260

265

270

275

gaa cct cca gga gac ttt cca ttt gaa gat tac agt caa cat ata tat 982

Glu Pro Pro Gly Asp Phe Pro Phe Glu Asp Tyr Ser Gln His Ile Tyr

280

285

290

aga acc att tct gat ggg act atc agt gca tcc aaa cag gag agt ggg 1030

Arg Thr Ile Ser Asp Gly Thr Ile Ser Ala Ser Lys Gln Glu Ser Gly

295

300

305

aag atg gat gcc aaa acc cca gta gga aag gcc aag ggc aaa ttg tgg 1078

Lys Met Asp Ala Lys Thr Pro Val Gly Lys Ala Lys Gly Lys Leu Trp

310

315

320

ctc ttt gga aag aag cca aag ggc cca gca cta gaa gat ttc agt cat 1126

Leu Phe Gly Lys Lys Pro Lys Gly Pro Ala Leu Glu Asp Phe Ser His

325

330

335

ctg cca cca gaa cag aga cgt aaa aaa cta cag cag cgc att gat gaa 1174

Leu Pro Pro Glu Gln Arg Arg Lys Lys Leu Gln Gln Arg Ile Asp Glu

340

345

350

355

ctt aac aga gaa cta cag aaa gaa tca gac caa aaa gat gca ctc aac 1222

Leu Asn Arg Glu Leu Gln Lys Glu Ser Asp Gln Lys Asp Ala Leu Asn

360

365

370

aaa atg aaa gat gta tat gag aag gat cca caa atg ggg gat cca ggg 1270

Lys Met Lys Asp Val Tyr Glu Lys Asp Pro Gln Met Gly Asp Pro Gly

375

380

385

agt ttg cag cct aaa tta gca gag acc atg aat aac att gac cgc cta 1318

Ser Leu Gln Pro Lys Leu Ala Glu Thr Met Asn Asn Ile Asp Arg Leu

390

395

400

cga atg gaa atc cat aag aat gag gct tgg ctc tct gaa gtc gaa ggc 1366

Arg Met Glu Ile His Lys Asn Glu Ala Trp Leu Ser Glu Val Glu Gly

405

410

415

aaa aca ggt ggg aga gga gac aga aga cat agc agt gac ata aat cat 1414

Lys Thr Gly Gly Arg Gly Asp Arg Arg His Ser Ser Asp Ile Asn His

420

425

430

435

ctt gta aca cag gga cga gaa agt cct gag gga agt tac act gat gat 1462

Leu Val Thr Gln Gly Arg Glu Ser Pro Glu Gly Ser Tyr Thr Asp Asp

440

445

450

gca aac cag gaa gtc cgt ggg cca ccc cag cag cat ggt cac cac aat 1510

Ala Asn Gln Glu Val Arg Gly Pro Pro Gln Gln His Gly His His Asn

455

460

465

gag ttt gat gat gaa ttt gag gat gat gat ccc ttg cct gct att gga 1558

Glu Phe Asp Asp Glu Phe Glu Asp Asp Asp Pro Leu Pro Ala Ile Gly

470

475

480

cac tgc aaa gct atc tac cct ttt gat gga cat aat gaa ggt act cta 1606

His Cys Lys Ala Ile Tyr Pro Phe Asp Gly His Asn Glu Gly Thr Leu

485

490

495

gca atg aaa gaa ggt gaa gtt ctc tac att ata gag gag gac aaa ggt 1654

Ala Met Lys Glu Gly Glu Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly

500 505 510 515

gac gga tgg aca aga gct cgg aga cag aac ggt gaa gaa ggc tac gtt 1702

Asp Gly Trp Thr Arg Ala Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val

520 525 530

ccc acg tca tac ata gat gta act cta gag aaa aac agt aaa ggt tcc 1750

Pro Thr Ser Tyr Ile Asp Val Thr Leu Glu Lys Asn Ser Lys Gly Ser

535 540 545

tgaagagggt ttctgaggaa atgggcaaga tgttgaagga gggtacatgc agctgctttt 1810

gggggagggt attagagttg tcaggctcaa agagagtgag agaagcaagt tgcattgagt 1870

catgcagaca tgattttttt ttactaact tcattagcat ttccatacat tgtttttaaa 1930

aatcataata ccaaccctta agttcctagt tcacagttat tcccacaaaa gaaaaagcca 1990

acaatagtgt accatttttc tattttattt tattgctgtc taatcaataa agaatgcaga 2050

gctgtcaaaa aatgtgtctt acatttagct gtcccaacag gattgtcttc cctcccagct 2110

ctgggttttaa ttggctttta gaccactat ctgtcagatc cttgccatct gtcagtgtct 2170

gcctgcgcca cctccgtgct tgcctaacat cctgttgcac gtctagcgtg attgagcnag 2230

attttcaggc atgtcttttag aatcccctgg tncgtgtcaaa gcctgggttg gtttacattg 2290

gtngtgcaat cnccttgtca acatctccag cactatngtt cctcttagg tn 2342

<210> 4

<211> 547

<212> PRT

<213> Homo sapiens

<400> 4

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His Thr Gln Trp Gly Ile Asp Phe Leu Glu Arg Tyr Ala Lys Phe Val

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Lys Glu Arg Ile Glu Ile Glu Gln Asn Tyr Ala Lys Gln Leu Arg Asn

35 40 45

Leu Val Lys Lys Tyr Cys Pro Lys Arg Ser Ser Lys Asp Glu Glu Pro

50

55

60

Arg Phe Thr Ser Cys Val Ala Phe Phe Asn Ile Leu Asn Glu Leu Asn

65

70

75

80

Asp Tyr Ala Gly Gln Arg Glu Val Val Ala Glu Glu Met Ala His Arg

85

90

95

Val Tyr Gly Glu Leu Met Arg His Ala His Asp Leu Lys Thr Glu Arg

100

105

110

Lys Met His Leu Gln Glu Gly Arg Lys Ala His Gln Ser Leu Ala Met

115

120

125

Cys Trp Asn Gln Met Asp Asn Ser Lys Lys Lys Phe Glu Arg Glu Cys

130

135

140

Arg Glu Ala Glu Lys Ala His Gln Ser Tyr Glu Arg Leu Asp Asn Asp

145

150

155

160

Thr Asn Ala Thr Lys Ala Asp Val Glu Asn Ala Lys Gln Gln Leu Asn

165

170

175

Leu Arg Thr His Met Ala Asp Glu Asn Lys Asn Ala Tyr Ala Ala Gln

180

185

190

Leu Gln Asn Phe Asn Gly Glu Gln His Lys His Phe Tyr Val Val Ile

195

200

205

Pro Gln Ile Tyr Lys Gln Leu Gln Glu Met Asp Glu Arg Arg Thr Ile

210

215

220

Lys Leu Ser Glu Cys Tyr Arg Gly Phe Ala Asp Ser Glu Arg Lys Val

225

230

235

240

Ile Pro Ile Ile Ser Lys Cys Leu Glu Gly Met Ile Leu Ala Ala Lys

245

250

255

Ser Val Asp Glu Arg Arg Asp Ser Gln Met Val Val Asp Ser Phe Lys

260

265

270

Ser Gly Phe Glu Pro Pro Gly Asp Phe Pro Phe Glu Asp Tyr Ser Gln

275

280

285

His Ile Tyr Arg Thr Ile Ser Asp Gly Thr Ile Ser Ala Ser Lys Gln

290

295

300

Glu Ser Gly Lys Met Asp Ala Lys Thr Pro Val Gly Lys Ala Lys Gly

305 310 315 320

Lys Leu Trp Leu Phe Gly Lys Lys Pro Lys Gly Pro Ala Leu Glu Asp

325 330 335

Phe Ser His Leu Pro Pro Glu Gln Arg Arg Lys Lys Leu Gln Gln Arg

340 345 350

Ile Asp Glu Leu Asn Arg Glu Leu Gln Lys Glu Ser Asp Gln Lys Asp

355 360 365

Ala Leu Asn Lys Met Lys Asp Val Tyr Glu Lys Asp Pro Gln Met Gly

370 375 380

Asp Pro Gly Ser Leu Gln Pro Lys Leu Ala Glu Thr Met Asn Asn Ile

385 390 395 400

Asp Arg Leu Arg Met Glu Ile His Lys Asn Glu Ala Trp Leu Ser Glu

405 410 415

Val Glu Gly Lys Thr Gly Gly Arg Gly Asp Arg Arg His Ser Ser Asp

420 425 430

Ile Asn His Leu Val Thr Gln Gly Arg Glu Ser Pro Glu Gly Ser Tyr

435

440

445

Thr Asp Asp Ala Asn Gln Glu Val Arg Gly Pro Pro Gln Gln His Gly

450

455

460

His His Asn Glu Phe Asp Asp Glu Phe Glu Asp Asp Asp Pro Leu Pro

465

470

475

480

Ala Ile Gly His Cys Lys Ala Ile Tyr Pro Phe Asp Gly His Asn Glu

485

490

495

Gly Thr Leu Ala Met Lys Glu Gly Glu Val Leu Tyr Ile Ile Glu Glu

500

505

510

Asp Lys Gly Asp Gly Trp Thr Arg Ala Arg Arg Gln Asn Gly Glu Glu

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Gly Tyr Val Pro Thr Ser Tyr Ile Asp Val Thr Leu Glu Lys Asn Ser

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535

540

Lys Gly Ser

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<210> 5

<211> 711

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (143)..(487)

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acgtgcctc ctgcctgcag cc atg acg ccc tgc tca cct gat ctg gtg gtc 172

Met Thr Pro Cys Ser Pro Asp Leu Val Val

1

5

10

ctc atg ggc tta cct ctg gcc cag gcc ttg gac tgc cac gtg tgt gcc 220

Leu Met Gly Leu Pro Leu Ala Gln Ala Leu Asp Cys His Val Cys Ala

15

20

25

tac aac gga gac aac tgc ttc aac ccc atg cgc tgc ccg gct atg gtt 268

Tyr Asn Gly Asp Asn Cys Phe Asn Pro Met Arg Cys Pro Ala Met Val

30

35

40

gcc tac tgc atg acc acg cgc acc tac tac acc ccc acc agg atg aag 316

Ala Tyr Cys Met Thr Thr Arg Thr Tyr Tyr Thr Pro Thr Arg Met Lys

45

50

55

gtc agt aag tcc tgc gtg ccc cgc tgc ttc gag act gtg tat gat ggc 364

Val Ser Lys Ser Cys Val Pro Arg Cys Phe Glu Thr Val Tyr Asp Gly

60

65

70

tac tcc aag cac gcg tcc acc acc tcc tgc tgc cag tac gac ctc tgc 412

Tyr Ser Lys His Ala Ser Thr Thr Ser Cys Cys Gln Tyr Asp Leu Cys

75

80

85

90

aac ggc acc ggc ctt gcc acc ccg gcc acc ctg gcc ctg gcc ccc atc 460

Asn Gly Thr Gly Leu Ala Thr Pro Ala Thr Leu Ala Leu Ala Pro Ile

95

100

105

ctc ctg gcc acc ctc tgg ggt ctc ctc taaagccccc gaggcagacc 507

Leu Leu Ala Thr Leu Trp Gly Leu Leu

110

115

cactcaagaa caaagctctc gagacacact gctacaccct cgcacccagc tcaccctgcc 567

tcaccctcca cactccctgc gacctcctca gccatgccca gggtcaggac tgtgggcaag 627

aagacacccg acctcccca accaccacac gacctcactt cgaggccttg acctttaaat 687

aaaaaaaaa aaaaaaaaaa aaaa 711

<210> 6

<211> 115

<212> PRT

<213> Homo sapiens

<400> 6

Met Thr Pro Cys Ser Pro Asp Leu Val Val Leu Met Gly Leu Pro Leu

1 5 10 15

Ala Gln Ala Leu Asp Cys His Val Cys Ala Tyr Asn Gly Asp Asn Cys

20 25 30

Phe Asn Pro Met Arg Cys Pro Ala Met Val Ala Tyr Cys Met Thr Thr

35 40 45

Arg Thr Tyr Tyr Thr Pro Thr Arg Met Lys Val Ser Lys Ser Cys Val

50

55

60

Pro Arg Cys Phe Glu Thr Val Tyr Asp Gly Tyr Ser Lys His Ala Ser

65

70

75

80

Thr Thr Ser Cys Cys Gln Tyr Asp Leu Cys Asn Gly Thr Gly Leu Ala

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90

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Thr Pro Ala Thr Leu Ala Leu Ala Pro Ile Leu Leu Ala Thr Leu Trp

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105

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Gly Leu Leu

115

<210> 7

<211> 1987

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (991) .. (1446)

<220>

<221> variation

<222> (1)..(1981)

<223> where n can be any nucleotide

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ggcaacatca agaccctagg agacgcctat gagtttgagg tggacgtgag agacttctca 120

cctgaagaca tcattgtcac cacctccaaa caaccaaca tcgaggtgag gggctgagaa 180

agctggcggc tgaacggaca ctgtacatga aacaccttac gactacacaa gtgccagact 240

gccggaggac gtggaccccg agcgtgcggt gacctcggct actgtcggga ggacggacag 300

cctcactagt ccgggcacgc gtcacccgca tacagaacac gtccagcaga ccttcaggac 360

ggagatcaaa atctgagtgc ctctcccttc cctttccctg tccccccgcc ccacgcctgc 420

cagcaaagcc tcgctaacc cattacaaca gctccaggac atctcagccc aggttctagc 480

ccccacgcac ccagacccc aggtggacca tcctcccaaa ctagggccct ccactctatc 540

cagggcaggc cagggactcc ctggcctgac acatgatgcc cagatttcag atttggcctc 600

cgtcacttaa tccagagtac aggggctggg gtcaggggaag gaagatctaa agaaccact 660

gtgggtcagg ggaatgggac cagcaggaca tatgggcaag ctctgcagga cagacagaca 720

gacaaaccct ctgatctatg aagtctctgc agggcaaggg gaccagggac ctggaaccct 780

cttggccaag gggagtggga gagacagagg gaaggtcaca ggcaaggggtg cctatctaag 840

tggaactaat tgcccgaggg ctgagcaagg ccaagaggag acagccgtga cggtaaactt 900

cccctctacc agcctccaag cccacgcca gcgagcaggc tgccctgccca ccccgcgccc 960

ccagccagct ggctgtgcca gggcagagcc atg cca cat ctg tat ata gat ggg 1014

Met Pro His Leu Tyr Ile Asp Gly

1

5

gtt ttt cca ata cag ctg gtt cgt gaa aaa ctg cat gaa act cct gcc 1062

Val Phe Pro Ile Gln Leu Val Arg Glu Lys Leu His Glu Thr Pro Ala

10

15

20

gtc ctg cgc ctg ctg ggg cct cca ggc aag gcc aag tgg ggt tgg ggg 1110

Val Leu Arg Leu Leu Gly Pro Pro Gly Lys Ala Lys Trp Gly Trp Gly

25 30 35 40

tgg ggc tgg tcc ttc tcc ctc cca cag gcc tgt gtt cnt ggg gct gct 1158

Trp Gly Trp Ser Phe Ser Leu Pro Gln Ala Cys Val Xaa Gly Ala Ala

45 50 55

ccc atg cag aca gga tca cct aac aga gat gga agc cag ggc atg gat 1206

Pro Met Gln Thr Gly Ser Pro Asn Arg Asp Gly Ser Gln Gly Met Asp

60 65 70

ggg gct ttg ggt cct cga ggt tgg acc cca gct tct tgc cac ctt ccc 1254

Gly Ala Leu Gly Pro Arg Gly Trp Thr Pro Ala Ser Cys His Leu Pro

75 80 85

ctc cgg cag tca gct ctc cat cca tcc ccc tct tta atc tat gaa tct 1302

Leu Arg Gln Ser Ala Leu His Pro Ser Pro Ser Leu Ile Tyr Glu Ser

90 95 100

ata ggc tcg gtg tgt gta aca aca cac ccc tat cgt tgt cct tca aat 1350

Ile Gly Ser Val Cys Val Thr Thr His Pro Tyr Arg Cys Pro Ser Asn

105 110 115 120

act cag cat tac cat tgg ttg agg cca aat tca gag ctt tct caa atc 1398

Thr Gln His Tyr His Trp Leu Arg Pro Asn Ser Glu Leu Ser Gln Ile

125

130

135

aga ttt aca atc tcc att ttc att aac ggg gaa aca tcc ccg agc cac 1446

Arg Phe Thr Ile Ser Ile Phe Ile Asn Gly Glu Thr Ser Pro Ser His

140

145

150

tgagtgtgt gctttgtcac tgaaggtag atctgaaccc aggggtgtcaa cngctgtct 1506

caactcccca cctctgggca ctgaggagta tttcccctca ttctacctct ctaaggctat 1566

gcacccctcc ccacgtcttc cagctggggg atggggggag tcataggaaa agccccatc 1626

tcccatctgg gatagggacc ttccatcagc cttaaccctg ggaaatgcct gctgccccca 1686

gtgactcttg gtttcgtctc ccacatacag aagcaggggtg gaggggaagg gtgggtctca 1746

gtagcaggg gtccccaggg caagtcagcc tcctccctcc atgcctctct ggtcagtgtg 1806

ccttaggggtg gcctctcact ccaccactc tgggcccttg ggggaggact ggggaggggg 1866

ccgtgggaga gccctgacgc tggaacctgt atacacaata aaggacagtc tcacagacnt 1926

ctggaggccg cctgccngga gttctcaaac ttagggcagg gcnnnnctta cttgagagaa 1986

a

1987

<210> 8

<211> 152

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)..(152)

<223> where Xaa can any amino acid

<400> 8

Met Pro His Leu Tyr Ile Asp Gly Val Phe Pro Ile Gln Leu Val Arg

1

5

10

15

Glu Lys Leu His Glu Thr Pro Ala Val Leu Arg Leu Leu Gly Pro Pro

20

25

30

Gly Lys Ala Lys Trp Gly Trp Gly Trp Gly Trp Ser Phe Ser Leu Pro

35

40

45

Gln Ala Cys Val Xaa Gly Ala Ala Pro Met Gln Thr Gly Ser Pro Asn

50

55

60

Arg Asp Gly Ser Gln Gly Met Asp Gly Ala Leu Gly Pro Arg Gly Trp

65

70

75

80

Thr Pro Ala Ser Cys His Leu Pro Leu Arg Gln Ser Ala Leu His Pro

85

90

95

Ser Pro Ser Leu Ile Tyr Glu Ser Ile Gly Ser Val Cys Val Thr Thr

100

105

110

His Pro Tyr Arg Cys Pro Ser Asn Thr Gln His Tyr His Trp Leu Arg

115

120

125

Pro Asn Ser Glu Leu Ser Gln Ile Arg Phe Thr Ile Ser Ile Phe Ile

130

135

140

Asn Gly Glu Thr Ser Pro Ser His

145

150

<210> 9

<211> 1395

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (587)..(1342)

<220>

<221> variation

<222> (1)..(1395)

<223> where n can be any nucleotide

<400> 9

tgtgtgtgtg tgtgtgtgtg tgcgcgtgtg tgtgtgcacg cgtgcgtgcg tgtgtgcacg 60

tgcnngtgtg tgtgtggttg gcaggcctag tgatcctgtt gtttagtgtc tctgagattt 120

gagttgtgcc tttttacttt gcataaagta gatacttggc catatgtagt tccaaggaga 180

agtcagagtt ccacctttgg agtctttcct tctgattcac gatatttcttt caacaatttt 240

ccacttagga atccatcaca aaagttttgc acatgctcta cggaaacttc tgctgtgggc 300

agtgatatccc actcgtcac tagagtctgg taaattgcc aagctggcag ttgagactcc 360

tttagtttga aaaatgatat caccttccca ttttctttca taccactgtc caccagaata 420

aagagaatct tcccctggaa gagcttggct gccttctggt atctgtgcat gttctctcca 480

tactctgggg aggcttgtt cattatcagg aggagatgat tctgaattac gctggtgaat 540

aacccaatca cagtcacagg gttggagcag gagcaggaga gggaca atg gaa gct 595

Met Glu Ala

1

gcc ccg tcc agg ttc atg ttc ctc tta ttt ctc ctc acg tgt gag ctg 643

Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu Thr Cys Glu Leu

5

10

15

gct gca gaa gtt gct gca gaa gtt gag aaa tcc tca gat ggt cct ggt 691

Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser Ser Asp Gly Pro Gly

20

25

30

35

gct gcc cag gaa ccc acg tgg ctc aca gat gtc cca gct gcc atg gaa 739

Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp Val Pro Ala Ala Met Glu

40

45

50

ttc att gct gcc act gag gtg gct gtc ata ggc ttc ttc cag gat tta 787

Phe Ile Ala Ala Thr Glu Val Ala Val Ile Gly Phe Phe Gln Asp Leu

55

60

65

gaa ata cca gca gtg ccc ata ctc cat agc atg gtg caa aaa ttc cca 835

Glu Ile Pro Ala Val Pro Ile Leu His Ser Met Val Gln Lys Phe Pro

70

75

80

ggc gtg tca ttt ggg atc agc act gat tct gag gtt ctg aca cac tac 883

Gly Val Ser Phe Gly Ile Ser Thr Asp Ser Glu Val Leu Thr His Tyr

85

90

95

aac atc act ggg aac acc atc tgc ctc ttt cgc ctg gta gac aat gaa 931

Asn Ile Thr Gly Asn Thr Ile Cys Leu Phe Arg Leu Val Asp Asn Glu

100

105

110

115

caa ctg aat tta gag gac gaa gac att gaa agc att gat gcc acc aaa 979

Gln Leu Asn Leu Glu Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys

120

125

130

ttg agc cgt ttc att gag atc aac agc ctc cac atg gtg aca gag tac 1027

Leu Ser Arg Phe Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr

135

140

145

aac cct gtg act gtg att ggg tta ttc aac agc gta att cag att cat . 1075

Asn	Pro	Val	Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	
		150					155						160			
ctc	ctc	ctg	ata	atg	aac	aag	gcc	tcc	cca	gag	tat	gaa	gag	aac	atg	1123
Leu	Leu	Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	
		165					170						175			
cac	aga	tac	cag	aag	gca	gcc	aag	ctc	ttc	cag	ggg	aag	att	ctc	ttt	1171
His	Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	
180				185					190					195		
att	ctg	gtg	gac	agt	ggg	atg	aaa	gaa	aat	ggg	aag	gtg	ata	tca	ttt	1219
Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser	Phe	
			200					205					210			
ttc	aaa	cta	aag	gag	tct	cga	ctg	cca	gct	ttg	gga	att	tac	cag	act	1267
Phe	Lys	Leu	Lys	Glu	Ser	Arg	Leu	Pro	Ala	Leu	Gly	Ile	Tyr	Gln	Thr	
			215					220					225			
cta	gat	gac	gag	tgg	gat	aca	ctg	ccc	aca	gca	gaa	gtt	tcc	gta	gag	1315
Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val	Ser	Val	Glu	
			230					235					240			
cat	gtg	caa	aac	ttt	tgt	gat	gga	ttc	taagtgggaa	attggtgaaa						1362

His Val Gln Asn Phe Cys Asp Gly Phe

245

250

gaaaatcgtg aatcaggaag ggggaaaagg gac

1395

<210> 10

<211> 252

<212> PRT

<213> Homo sapiens

<400> 10

Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu Thr

1

5

10

15

Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser Ser Asp

20

25

30

Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp Val Pro Ala

35

40

45

Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val Ile Gly Phe Phe

50

55

60

Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu His Ser Met Val Gln

65

70

75

80

Lys Phe Pro Gly Val Ser Phe Gly Ile Ser Thr Asp Ser Glu Val Leu

85

90

95

Thr His Tyr Asn Ile Thr Gly Asn Thr Ile Cys Leu Phe Arg Leu Val

100

105

110

Asp Asn Glu Gln Leu Asn Leu Glu Asp Glu Asp Ile Glu Ser Ile Asp

115

120

125

Ala Thr Lys Leu Ser Arg Phe Ile Glu Ile Asn Ser Leu His Met Val

130

135

140

Thr Glu Tyr Asn Pro Val Thr Val Ile Gly Leu Phe Asn Ser Val Ile

145

150

155

160

Gln Ile His Leu Leu Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu

165

170

175

Glu Asn Met His Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys

180

185

190

Ile Leu Phe Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val

195

200

205

Ile Ser Phe Phe Lys Leu Lys Glu Ser Arg Leu Pro Ala Leu Gly Ile

210

215

220

Tyr Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val

225

230

235

240

Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe

245

250

<210> 11

<211> 1481

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (183)..(1361)

<220>

<221> variation

<222> (1)..(1481)

<223> where n can be any nucleotide

<400> 11

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agccagtggg catggaatgg gctgggggtca aagactgggt gcctgggagc tgaggcagcc 120

accgtttcag cctggccagc cctctggacc ccgaggttgg accctactgt gacacaccta 180

cc atg cgg aca ctc ttc aac ctc ctc tgg ctt gcc ctg gcc tgc agc 227

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser

1 5 10 15

cct gtt cac act acc ctg tca aag tca gat gcc aaa aaa gcc gcc tca 275

Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser

20 25 30

aag acg ctg ctg gag aag agt cag ttt tca gat aag ccg gtg caa gac 323

Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp

35 40 45

cgg ggt ttg gtg gtg acg gac ctc aaa gct gag agt gtg gtt ctt gag 371

Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu

50	55	60	
cat cgc agc tac tgc tcg gca aag gcc cgg gac aga cac ttt gct ggg 419			
His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly			
65	70	75	
gat gta ctg ggc tat gtc act cca tgg aac agc cat ggc tac gat gtc 467			
Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val			
80	85	90	95
acc aag gtc ttt ggg agc aag ttc aca cag atc tca ccc gtc tgg ctg 515			
Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu			
100	105	110	
cag ctg aag aga cgt ggc cgt gag atg ttt gag gtc acg ggc ctc cac 563			
Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His			
115	120	125	
gac gtg gac caa ggg tgg atg cga gct gtc agg aag cat gcc aag ggc 611			
Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly			
130	135	140	
ctg cac ata gtg cct cgg ctc cta ttt gag gac tgg act tac gat gat 659			
Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp			

145	150	155	
ttc cgg aac gtc tta gac agt gag gat gag ata gag gag ctg agc aag 707			
Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys			
160	165	170	175
acc gtg gtc cag gtg gca aag aac cag cat ttc gat ggc ttc gtg gtg 755			
Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val			
	180	185	190
gag gtc tgg aac cag ctg cta agc cag aag cgc gtg ggc ctc atc cac 803			
Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His			
	195	200	205
atg ctc acc cac ttg gcc gag gct ctg cac cag gcc cgg ctg ctg gcc 851			
Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala			
	210	215	220
ctc ctg gtc atc ccg cct gca atc acc ccc ggg acc gac cag ctg ggc 899			
Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly			
	225	230	235
atg ttc acg cac aag gag ttt gag cag ctg gcc ccc gtg ctg gat ggt 947			
Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly			

240	245	250	255	
ttc agc ctc atg acc tac gac tac tct aca gcg cat cag cct ggc cct				995
Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro				
	260	265	270	
aat gca ccc ctg tcc tgg gtt cga gcc tgc gtc cag gtc ctg gac ccg				1043
Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro				
	275	280	285	
aag tcc aag tgg cga agc aaa atc ctc ctg ggg ctc aac ttt tat ggt				1091
Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly				
	290	295	300	
atg gac tac gcg acc tcc aag gat gcc cgt gag cct gtt gtc ggg gcc				1139
Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala				
	305	310	315	
agg tac atc cag aca ctg aag gac cac agg ccc cgg atg gtg tgg gac				1187
Arg Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp				
320	325	330	335	
agc cag gcc tca gag cac ttc ttc gag tac aag aag agc cgc agt ggg				1235
Ser Gln Ala Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly				

340

345

350

agg cac gtc gtc ttc tac cca acc ctg aag tcc ctg cag gtg cgg ctg 1283

Arg His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu

355

360

365

gag ctg gcc cgg gag ctg ggc gtt ggg gtc tct atc tgg gag ctg ggc 1331

Glu Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Gly

370

375

380

cag ggc ctg gac tac ttc tac gac ctg ctc taggtgggca ttgcggcctc 1381

Gln Gly Leu Asp Tyr Phe Tyr Asp Leu Leu

385

390

cgcggtggac gtgttctttt ctaagccatg gagtgagtga gcaggtgtga aatacaggcc 1441

tccactccgt ttgctgtgaa aaaaaaaaaa aaaaaaaaaa 1481

<210> 12

<211> 393

<212> PRT

<213> Homo sapiens

<400> 12

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro

1 5 10 15

Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys

20 25 30

Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg

35 40 45

Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His

50 55 60

Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp

65 70 75 80

Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr

85 90 95

Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln

100 105 110

Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp

115 120 125

Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu

130

135

140

His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe

145

150

155

160

Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr

165

170

175

Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu

180

185

190

Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met

195

200

205

Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu

210

215

220

Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met

225

230

235

240

Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe

245

250

255

Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn

260

265

270

Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys

275

280

285

Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly Met

290

295

300

Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala Arg

305

310

315

320

Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp Ser

325

330

335

Gln Ala Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg

340

345

350

His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu Glu

355

360

365

Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Gly Gln

370

375

380

Gly Leu Asp Tyr Phe Tyr Asp Leu Leu

385

390

<210> 13

<211> 811

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(486)

<400> 13

ccgccagcg ggtggaactc gggtagccc actccagctt tttccgaagg ccgccagggc 60

ctacccccaa gcccccccca gggcgcgggc atg ctc atg ggt tgc gct ggg ccc 114

Met Leu Met Gly Cys Ala Gly Pro

1

5

gga aag cat gcg cag cgg ctg gcc tgc ctt ccg ccc cgg gcc ctt tgc 162

Gly Lys His Ala Gln Arg Leu Ala Cys Leu Pro Pro Arg Ala Leu Cys

10

15

20

cca gaa gga tgg agc cct ttg cat tct ttt cgt cac ctc att tat tta 210

Pro Glu Gly Trp Ser Pro Leu His Ser Phe Arg His Leu Ile Tyr Leu

25 30 35 40

att ttt ttt ttt atg ttg gat gta gtt ttt ttt tct gtt gca att gtg 258

Ile Phe Phe Phe Met Leu Asp Val Val Phe Phe Ser Val Ala Ile Val

45 50 55

gca aat ata cat gtc cgc tgt ccc cag ttc cag cga caa caa aaa gac 306

Ala Asn Ile His Val Arg Cys Pro Gln Phe Gln Arg Gln Gln Lys Asp

60 65 70

aac ccc aac ctc ctc cag atg cac agt gtg tgt cac gcg tgt ctg gac 354

Asn Pro Asn Leu Leu Gln Met His Ser Val Cys His Ala Cys Leu Asp

75 80 85

tgt gaa gac atg cac ata gcg agc cta tac ggt tct aaa ggt cac tgg 402

Cys Glu Asp Met His Ile Ala Ser Leu Tyr Gly Ser Lys Gly His Trp

90 95 100

agg gcg tgg ttt ctg tac cag ggc caa atc cca gca ccc agt acc ctg 450

Arg Ala Trp Phe Leu Tyr Gln Gly Gln Ile Pro Ala Pro Ser Thr Leu

105 110 115 120

cac acc cac cgc cct gtg ccc tgc atg tgg aaa tgc tgagagaacg 496

His Thr His Arg Pro Val Pro Cys Met Trp Lys Cys

125

130

tgctccagtt cgggcctccc cagccccctcc cactggaag ggcaggtctg gtcccccttg 556

tcattgctcc tcaccactg ctgtctccaa ccccaaatag gagagtgacg gccacctggg 616

cagctcttct ttggagcatg catcctgctt ggccggctcc tcctcctcct ccagccagtg 676

ggagcacttt acttgctgta ttttcctgtg acctcccatg accgcagggg tgaagtcaat 736

gacgcagttc ctccaattgc tactaagcca aaaccagtc ccagccttgc tcagatccct 796

ggaacacagt tagtg 811

<210> 14

<211> 132

<212> PRT

<213> Homo sapiens

<400> 14

Met Leu Met Gly Cys Ala Gly Pro Gly Lys His Ala Gln Arg Leu Ala

1 5 10 15

Cys Leu Pro Pro Arg Ala Leu Cys Pro Glu Gly Trp Ser Pro Leu His

20 25 30

Ser Phe Arg His Leu Ile Tyr Leu Ile Phe Phe Phe Met Leu Asp Val

35 40 45

Val Phe Phe Ser Val Ala Ile Val Ala Asn Ile His Val Arg Cys Pro

50 55 60

Gln Phe Gln Arg Gln Gln Lys Asp Asn Pro Asn Leu Leu Gln Met His

65 70 75 80

Ser Val Cys His Ala Cys Leu Asp Cys Glu Asp Met His Ile Ala Ser

85 90 95

Leu Tyr Gly Ser Lys Gly His Trp Arg Ala Trp Phe Leu Tyr Gln Gly

100 105 110

Gln Ile Pro Ala Pro Ser Thr Leu His Thr His Arg Pro Val Pro Cys

115 120 125

Met Trp Lys Cys

130

<210> 15

<211> 734

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (146)..(460)

<220>

<221> variation

<222> (1)..(734)

<223> where n can be any nucleotide

<400> 15

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cgaagngccc catggggggg atnttacgga aaactaataa gatncaaaga annattacct 120

accttgataa aattnccttt aatga atg aac acc aca ctc agg ata aaa tcc 172

Met Asn Thr Thr Leu Arg Ile Lys Ser

1

5

aaa ctc cct act tct gca tat gtg gct ttc tgt gac ctg gct tgt gcc 220

Lys Leu Pro Thr Ser Ala Tyr Val Ala Phe Cys Asp Leu Ala Cys Ala

10

15

20

25

cgt tcc cct agc tgc tcc cca atc tgg tct cct acc atg tca ctc tct 268

Arg Ser Pro Ser Cys Ser Pro Ile Trp Ser Pro Thr Met Ser Leu Ser

30

35

40

gtg tgc cac cca tgc tgg tct ctt tcc agt tca agc cca tcc agc ctc 316

Val Cys His Pro Cys Trp Ser Leu Ser Ser Ser Ser Pro Ser Ser Leu

45

50

55

tgg gct ttt ctc tgc ctt ttt ttg ttg ttc cct cct ccc gga atg ctt 364

Trp Ala Phe Leu Cys Leu Phe Leu Leu Phe Pro Pro Pro Gly Met Leu

60

65

70

ttc cca ggg tct ccc atg gct gac ttc tct ggc ctg agg gct cca ttc 412

Phe Pro Gly Ser Pro Met Ala Asp Phe Ser Gly Leu Arg Ala Pro Phe

75

80

85

aaa tgt cac ctc ctt aca gga gcc ttc tct gat gat cta aaa ggt ctc 460

Lys Cys His Leu Leu Thr Gly Ala Phe Ser Asp Asp Leu Lys Gly Leu

90

95

100

105

taggaacttt tagtgtcttc ctgtaattct ctgtacattt cctgtgtttc cttattttatt 520

tactgtttga aacatagtca tagtagacaa taaatattaa actacgtgaa actagtttag 580

tatttataat attataactt atttagatat aattatgtta ttataataaa atatgtgaaa 640

cagctgcttt tgtaggggaa aaagttgaat attggccatt ccacatgggt cactgaagaa 700

ataataatgt tatcattaag tgtacttatt ggca

734

<210> 16

<211> 105

<212> PRT

<213> Homo sapiens

<400> 16

Met Asn Thr Thr Leu Arg Ile Lys Ser Lys Leu Pro Thr Ser Ala Tyr

1

5

10

15

Val Ala Phe Cys Asp Leu Ala Cys Ala Arg Ser Pro Ser Cys Ser Pro

	20		25		30
Ile	Trp	Ser	Pro	Thr	Met
Ser	Leu	Ser	Val	Cys	His
Pro	Cys	Trp	Ser		
35		40		45	
Leu	Ser	Ser	Ser	Ser	Pro
Ser	Ser	Leu	Trp	Ala	Phe
Leu	Cys	Leu	Phe		
50		55		60	
Leu	Leu	Phe	Pro	Pro	Pro
Gly	Met	Leu	Phe	Pro	Gly
Ser	Pro	Met	Ala		
65		70		75	
Asp	Phe	Ser	Gly	Leu	Arg
Ala	Pro	Phe	Lys	Cys	His
Leu	Leu	Thr	Gly		
85		90		95	
Ala	Phe	Ser	Asp	Asp	Leu
Lys	Gly	Leu			
100		105			

<210> 17

<211> 1659

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (244)..(1473)

<400> 17

ctagaattca gcggccgctg aattctagtt tgctcccaaa ggcgcaccaa tgaccaacat 60

ttgccccccg gaggaagaa ctggaaccag cctctgacct gtccaggtgc cctgtccagc 120

tgactgcaag gacagagagg agtcctgccc agctcttgga tcagtctgct ggccgaggag 180

cccgggtggag ccaggggtga ccctggagcc cagcctgccc cgaggaggcc ccggctcaga 240

gcc atg cca ggt gtc tgt gat agg gcc cct gac ttc ctc tcc ccg tct 288

Met Pro Gly Val Cys Asp Arg Ala Pro Asp Phe Leu Ser Pro Ser

1 5 10 15

gaa gac cag gtg ctg agg cct gcc ttg ggc agc tca gtg gct ctg aac 336

Glu Asp Gln Val Leu Arg Pro Ala Leu Gly Ser Ser Val Ala Leu Asn

20 25 30

tgc acg gct tgg gta gtc tct ggg ccc cac tgc tcc ctg cct tca gtc 384

Cys Thr Ala Trp Val Val Ser Gly Pro His Cys Ser Leu Pro Ser Val

35 40 45

cag tgg ctg aaa gac ggg ctt cca ttg gga att ggg ggc cac tac agc 432

Gln Trp Leu Lys Asp Gly Leu Pro Leu Gly Ile Gly Gly His Tyr Ser

50

55

60

ctc cac gag tac tcc tgg gtc aag gcc aac ctg tca gag gtg ctt gtg 480

Leu His Glu Tyr Ser Trp Val Lys Ala Asn Leu Ser Glu Val Leu Val

65

70

75

tcc agt gtc ctg ggg gtc aac gtg acc agc act gaa gtc tat ggg gcc 528

Ser Ser Val Leu Gly Val Asn Val Thr Ser Thr Glu Val Tyr Gly Ala

80

85

90

95

ttc acc tgc tcc atc cag aac atc agc ttc tcc tcc ttc act ctt cag 576

Phe Thr Cys Ser Ile Gln Asn Ile Ser Phe Ser Ser Phe Thr Leu Gln

100

105

110

aga gct ggc cct aca agc cac gtg gct gcg gtg ctg gcc tcc ctc ctg 624

Arg Ala Gly Pro Thr Ser His Val Ala Ala Val Leu Ala Ser Leu Leu

115

120

125

gtc ctg ctg gcc ctg ctg ctg gcc gcc ctg ctc tat gtc aag tgc cgt 672

Val Leu Leu Ala Leu Leu Leu Ala Ala Leu Leu Tyr Val Lys Cys Arg

130

135

140

ctc aac gtg ctg ctc tgg tac cag gac gcg tat ggg gag gtg gag ata 720

Leu Asn Val Leu Leu Trp Tyr Gln Asp Ala Tyr Gly Glu Val Glu Ile

145

150

155

aac gac ggg aag ctc tac gac gcc tac gtc tcc tac agc gac tgc ccc 768

Asn Asp Gly Lys Leu Tyr Asp Ala Tyr Val Ser Tyr Ser Asp Cys Pro

160

165

170

175

gag gac cgc aag ttc gtg aac ttc atc cta aag ccg cag ctg gag cgg 816

Glu Asp Arg Lys Phe Val Asn Phe Ile Leu Lys Pro Gln Leu Glu Arg

180

185

190

cgt cgg ggc tac aag ctc ttc ctg gac gac cgc gac ctc ctg ccc cgc 864

Arg Arg Gly Tyr Lys Leu Phe Leu Asp Asp Arg Asp Leu Leu Pro Arg

195

200

205

gct gag ccc tcc gcc gac ctc ttg gtg aac ctg agc cgc tgc cga cgc 912

Ala Glu Pro Ser Ala Asp Leu Leu Val Asn Leu Ser Arg Cys Arg Arg

210

215

220

ctc atc gtg gtg ctt tcg gac gcc ttc ctg agc cgg gcc tgg tgc agc 960

Leu Ile Val Val Leu Ser Asp Ala Phe Leu Ser Arg Ala Trp Cys Ser

225

230

235

cac agc ttc cgg gag ggc ctg tgc cgg ctg ctg gag ctc acc cgc aga 1008

His Ser Phe Arg Glu Gly Leu Cys Arg Leu Leu Glu Leu Thr Arg Arg

240 245 250 255

ccc atc ttc atc acc ttc gag ggc cag agg cgc gac ccc gcg cac ccg 1056

Pro Ile Phe Ile Thr Phe Glu Gly Gln Arg Arg Asp Pro Ala His Pro

260 265 270

gcg ctc cgc ctg ctg cgc cag cac cgc cac ctg gtg acc ttg ctg ctc 1104

Ala Leu Arg Leu Leu Arg Gln His Arg His Leu Val Thr Leu Leu Leu

275 280 285

tgg agg ccc ggc tcc gtg act cct tcc tcc gat ttt tgg aaa gaa gtg 1152

Trp Arg Pro Gly Ser Val Thr Pro Ser Ser Asp Phe Trp Lys Glu Val

290 295 300

cag ctg gcg ctg ccg cgg aag gtg cgg tac agg ccg gtg gaa gga gac 1200

Gln Leu Ala Leu Pro Arg Lys Val Arg Tyr Arg Pro Val Glu Gly Asp

305 310 315

ccc cag acg cag ctg cag gac gac aag gac ccc atg ctg att ctt cga 1248

Pro Gln Thr Gln Leu Gln Asp Asp Lys Asp Pro Met Leu Ile Leu Arg

320 325 330 335

ggc cga gtc cct gag ggc cgg gcc ctg gac tca gag gtg gac ccg gac 1296

Gly Arg Val Pro Glu Gly Arg Ala Leu Asp Ser Glu Val Asp Pro Asp

340

345

350

cct gag ggc gac ctg ggt gtc cgg ggg cct gtt ttt gga gag cca tca 1344

Pro Glu Gly Asp Leu Gly Val Arg Gly Pro Val Phe Gly Glu Pro Ser

355

360

365

gct cca ccg cac acc agt ggg gtc tcg ctg gga gag agc cgg agc agc 1392

Ala Pro Pro His Thr Ser Gly Val Ser Leu Gly Glu Ser Arg Ser Ser

370

375

380

gaa gtg gac gtc tcg gat ctc ggc tcg cga aac tac agt gcc cgc aca 1440

Glu Val Asp Val Ser Asp Leu Gly Ser Arg Asn Tyr Ser Ala Arg Thr

385

390

395

gac ttc tac tgc ctg gtg tcc aag gat gat atg tagctccac cccagagtgc 1493

Asp Phe Tyr Cys Leu Val Ser Lys Asp Asp Met

400

405

410

aggatcatag ggacagcggg gccagggcag cggcgctcgt cctctgctca acaggaccac 1553

aaccctgcc agcagccctg ggaccctgcc agcagccctg ggaaaaggct gtggcctcag 1613

ggcgccctccc agtgccagaa aataaagtc ttttggattc tgaaaa

1659

<210> 18

<211> 410

<212> PRT

<213> Homo sapiens

<400> 18

Met Pro Gly Val Cys Asp Arg Ala Pro Asp Phe Leu Ser Pro Ser Glu

1 5 10 15

Asp Gln Val Leu Arg Pro Ala Leu Gly Ser Ser Val Ala Leu Asn Cys

20 25 30

Thr Ala Trp Val Val Ser Gly Pro His Cys Ser Leu Pro Ser Val Gln

35 40 45

Trp Leu Lys Asp Gly Leu Pro Leu Gly Ile Gly Gly His Tyr Ser Leu

50 55 60

His Glu Tyr Ser Trp Val Lys Ala Asn Leu Ser Glu Val Leu Val Ser

65 70 75 80

Ser Val Leu Gly Val Asn Val Thr Ser Thr Glu Val Tyr Gly Ala Phe

85

90

95

Thr Cys Ser Ile Gln Asn Ile Ser Phe Ser Ser Phe Thr Leu Gln Arg

100

105

110

Ala Gly Pro Thr Ser His Val Ala Ala Val Leu Ala Ser Leu Leu Val

115

120

125

Leu Leu Ala Leu Leu Leu Ala Ala Leu Leu Tyr Val Lys Cys Arg Leu

130

135

140

Asn Val Leu Leu Trp Tyr Gln Asp Ala Tyr Gly Glu Val Glu Ile Asn

145

150

155

160

Asp Gly Lys Leu Tyr Asp Ala Tyr Val Ser Tyr Ser Asp Cys Pro Glu

165

170

175

Asp Arg Lys Phe Val Asn Phe Ile Leu Lys Pro Gln Leu Glu Arg Arg

180

185

190

Arg Gly Tyr Lys Leu Phe Leu Asp Asp Arg Asp Leu Leu Pro Arg Ala

195

200

205

Glu Pro Ser Ala Asp Leu Leu Val Asn Leu Ser Arg Cys Arg Arg Leu

210

215

220

Ile Val Val Leu Ser Asp Ala Phe Leu Ser Arg Ala Trp Cys Ser His

225

230

235

240

Ser Phe Arg Glu Gly Leu Cys Arg Leu Leu Glu Leu Thr Arg Arg Pro

245

250

255

Ile Phe Ile Thr Phe Glu Gly Gln Arg Arg Asp Pro Ala His Pro Ala

260

265

270

Leu Arg Leu Leu Arg Gln His Arg His Leu Val Thr Leu Leu Leu Trp

275

280

285

Arg Pro Gly Ser Val Thr Pro Ser Ser Asp Phe Trp Lys Glu Val Gln

290

295

300

Leu Ala Leu Pro Arg Lys Val Arg Tyr Arg Pro Val Glu Gly Asp Pro

305

310

315

320

Gln Thr Gln Leu Gln Asp Asp Lys Asp Pro Met Leu Ile Leu Arg Gly

325

330

335

Arg Val Pro Glu Gly Arg Ala Leu Asp Ser Glu Val Asp Pro Asp Pro

340

345

350

Glu Gly Asp Leu Gly Val Arg Gly Pro Val Phe Gly Glu Pro Ser Ala

355

360

365

Pro Pro His Thr Ser Gly Val Ser Leu Gly Glu Ser Arg Ser Ser Glu

370

375

380

Val Asp Val Ser Asp Leu Gly Ser Arg Asn Tyr Ser Ala Arg Thr Asp

385

390

395

400

Phe Tyr Cys Leu Val Ser Lys Asp Asp Met

405

410

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<212> DNA

<213> Homo sapiens

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<221> CDS

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<400> 19

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cccagctaatt tttttgtttt gttttttag agactgggtc tcaactgtgtt gccagggctg 180

gtcatgaact cctgggctca agtaatcccc gtgccttggc ctctgaaagt gttgggatta 240

caggcatgag ccaactgtgcc tggccaaaaa agagctcttt aaaaaataat tttgtagatt 300

gacaaatgtg actcttgtaa ttttattgaa catgaaaaaa cccaggaatc tttatttgat 360

attaaacatt tttaaaggca tctcagttgt tgttgtaata acacattaag agaagtagtg 420

gttttttatt tccaaccttt gtgcatatag ctatttaatg cctacatgga tggctattat 480

ttcacttttt tcagttatta tgaagagatt gggtttcatt catttgtaaa gtttcagcca 540

gactgccttt cacaaattga tttgtcaaaa ttgaatgtta atcttgacat cccagtgcgt 600

ttttgcccgc gaacaggcct ttgaatgaag ctgcaaacac acattatctg gttgttaatt 660

gttttacaga tgagaactgg actgatgacc aactgcttgg ttttaaacca tgcaatgaaa 720

accttattgc tggctgcaat ataatcaatg ggaaatgtga atgtaacacc attcgaacct 780

gcagcaatcc ctttgagttt ccaagtcagg at atg tgc ctt tca gct tta aag 833

Met Cys Leu Ser Ala Leu Lys

1 5

aga att gaa gaa gag aag cca gat tgc tcc aag gcc cgc tgt gaa gtc 881

Arg Ile Glu Glu Glu Lys Pro Asp Cys Ser Lys Ala Arg Cys Glu Val

10 15 20

cag ttc tct cca cgt tgt cct gaa gat tct gtt ctg atc gag ggt tat 929

Gln Phe Ser Pro Arg Cys Pro Glu Asp Ser Val Leu Ile Glu Gly Tyr

25 30 35

gct cct cct ggg gag tgc tgt ccc tta ccc agc cgc tgc gtg tgc aac 977

Ala Pro Pro Gly Glu Cys Cys Pro Leu Pro Ser Arg Cys Val Cys Asn

40 45 50 55

ccc gca ggc tgt ctg cgc aaa gtc tgc cag ccg gga aac ctg aac ata 1025

Pro Ala Gly Cys Leu Arg Lys Val Cys Gln Pro Gly Asn Leu Asn Ile

60 65 70

cta gtg tca aaa gcc tca ggg aag ccg gga gag tgc tgt gac ctc tat 1073

Leu Val Ser Lys Ala Ser Gly Lys Pro Gly Glu Cys Cys Asp Leu Tyr

75

80

85

gag tgc aaa cca gtt ttc ggc gtg gac tgc agg act gtg gaa tgc cct 1121

Glu Cys Lys Pro Val Phe Gly Val Asp Cys Arg Thr Val Glu Cys Pro

90

95

100

cct gtt cag cag acc gcg tgt ccc ccg gac agc tat gaa act caa gtc 1169

Pro Val Gln Gln Thr Ala Cys Pro Pro Asp Ser Tyr Glu Thr Gln Val

105

110

115

aga cta act gca gat ggt tgc tgt act ttg cca aca aga tgc gag tgt 1217

Arg Leu Thr Ala Asp Gly Cys Cys Thr Leu Pro Thr Arg Cys Glu Cys

120

125

130

135

ctc tct ggc tta tgt ggt ttc ccc gtg tgt gag gtg gga tcc act ccc 1265

Leu Ser Gly Leu Cys Gly Phe Pro Val Cys Glu Val Gly Ser Thr Pro

140

145

150

cgc ata gtc tct cgt ggc gat ggg aca cct gga aag tgc tgt gat gtc 1313

Arg Ile Val Ser Arg Gly Asp Gly Thr Pro Gly Lys Cys Cys Asp Val

155

160

165

ttt gaa tgt gtt aat gat aca aag cca gcc tgc gta ttt aac aat gtg 1361

Phe Glu Cys Val Asn Asp Thr Lys Pro Ala Cys Val Phe Asn Asn Val

170

175

180

gaa tat tat gat gga gac atg ttt cga atg gac aac tgt cgg ttc tgt 1409

Glu Tyr Tyr Asp Gly Asp Met Phe Arg Met Asp Asn Cys Arg Phe Cys

185

190

195

cga tgc caa ggg ggc gtt gcc atc tgc ttc act gcc cag tgt ggt gag 1457

Arg Cys Gln Gly Gly Val Ala Ile Cys Phe Thr Ala Gln Cys Gly Glu

200

205

210

215

ata aac tgc gag agg tac tac gtg ccc gaa gga gag tgc tgc cca gtg 1505

Ile Asn Cys Glu Arg Tyr Tyr Val Pro Glu Gly Glu Cys Cys Pro Val

220

225

230

tgt gaa gat cca gtg tat cct ttt aat aat ccc gct ggc tgc tat gcc 1553

Cys Glu Asp Pro Val Tyr Pro Phe Asn Asn Pro Ala Gly Cys Tyr Ala

235

240

245

aat ggc ctg atc ctt gcc cac gga gac cgg tgg cgg gaa gac gac tgc 1601

Asn Gly Leu Ile Leu Ala His Gly Asp Arg Trp Arg Glu Asp Asp Cys

250

255

260

aca ttc tgc cag tgc gtc aac ggt gaa cgc cac tgc gtt gcg acc gtc 1649

Thr Phe Cys Gln Cys Val Asn Gly Glu Arg His Cys Val Ala Thr Val

265

270

275

tgc gga cag acc tgc aca aac cct gtg aaa gtg cct ggg gag tgt tgc 1697

Cys Gly Gln Thr Cys Thr Asn Pro Val Lys Val Pro Gly Glu Cys Cys

280

285

290

295

cct gtg tgc gaa gaa cca acc atc atc aca gtt gat cca cct gca tgt 1745

Pro Val Cys Glu Glu Pro Thr Ile Ile Thr Val Asp Pro Pro Ala Cys

300

305

310

ggg gag tta tca aac tgc act ctg aca ggg aag gac tgc att aat ggt 1793

Gly Glu Leu Ser Asn Cys Thr Leu Thr Gly Lys Asp Cys Ile Asn Gly

315

320

325

ttc aaa cgc gat cac aat ggt tgt cgg acc tgt cag tgc ata aac acc 1841

Phe Lys Arg Asp His Asn Gly Cys Arg Thr Cys Gln Cys Ile Asn Thr

330

335

340

gag gaa cta tgt tca gaa cgt aaa caa ggc tgc acc ttg aac tgt ccc 1889

Glu Glu Leu Cys Ser Glu Arg Lys Gln Gly Cys Thr Leu Asn Cys Pro

345

350

355

ttc ggt ttc ctt act gat gcc caa aac tgt gag atc tgt gag tgc cgc 1937

Phe Gly Phe Leu Thr Asp Ala Gln Asn Cys Glu Ile Cys Glu Cys Arg

360 365 370 375

cca agg ccc aag aag tgc aga ccc ata atc tgt gac aag tat tgt cca 1985

Pro Arg Pro Lys Lys Cys Arg Pro Ile Ile Cys Asp Lys Tyr Cys Pro

380 385 390

ctt gga ttg ctg aag aat aag cac ggc tgt gac atc tgt cgc tgt aag 2033

Leu Gly Leu Leu Lys Asn Lys His Gly Cys Asp Ile Cys Arg Cys Lys

395 400 405

aaa tgt cca gag ctc tca tgc agt aag atc tgc ccc ttg ggt ttc cag 2081

Lys Cys Pro Glu Leu Ser Cys Ser Lys Ile Cys Pro Leu Gly Phe Gln

410 415 420

cag gac agt cgc ggc tgt ctt atc tgc aag tgc aga gag gcc tct gct 2129

Gln Asp Ser Arg Gly Cys Leu Ile Cys Lys Cys Arg Glu Ala Ser Ala

425 430 435

tca gct ggg cca ccc atc ctg tcg ggc act tgt ctc acc gtg gat ggt 2177

Ser Ala Gly Pro Pro Ile Leu Ser Gly Thr Cys Leu Thr Val Asp Gly

440 445 450 455

cat cat cat aaa aat gag gag agc tgg cac gat ggg tgc cgg gaa tgc 2225

His His His Lys Asn Glu Glu Ser Trp His Asp Gly Cys Arg Glu Cys

460

465

470

tac tgt ctc aat gga cgg gaa atg tgt gcc ctg atc acc tgc ccg gtg 2273

Tyr Cys Leu Asn Gly Arg Glu Met Cys Ala Leu Ile Thr Cys Pro Val

475

480

485

cct gcc tgt ggc aac ccc acc att cac cct gga cag tgc tgc cca tca 2321

Pro Ala Cys Gly Asn Pro Thr Ile His Pro Gly Gln Cys Cys Pro Ser

490

495

500

tgt gca gat gac ttt gtg gtg cag aag cca gag ctc agt act ccc tcc 2369

Cys Ala Asp Asp Phe Val Val Gln Lys Pro Glu Leu Ser Thr Pro Ser

505

510

515

att tgc cac gcc cct gga gga gaa tac ttt gtg gaa gga gaa acg tgg 2417

Ile Cys His Ala Pro Gly Gly Glu Tyr Phe Val Glu Gly Glu Thr Trp

520

525

530

535

aac att gac tcc tgt act cag tgc acc tgc cac agc gga cgg gtg ctg 2465

Asn Ile Asp Ser Cys Thr Gln Cys Thr Cys His Ser Gly Arg Val Leu

540

545

550

tgt gag aca gag gtg tgc cca ccg ctg ctc tgc cag aac ccc tca cgc 2513

Cys Glu Thr Glu Val Cys Pro Pro Leu Leu Cys Gln Asn Pro Ser Arg

555

560

565

acc cag gat tcc tgc tgc cca cag tgt aca gat caa cct ttt cgg cct 2561

Thr Gln Asp Ser Cys Cys Pro Gln Cys Thr Asp Gln Pro Phe Arg Pro

570

575

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tcc ttg tcc cgc aat aac agc gta cct aat tac tgc aaa aat gat gaa 2609

Ser Leu Ser Arg Asn Asn Ser Val Pro Asn Tyr Cys Lys Asn Asp Glu

585

590

595

ggg gat ata ttc ctg gca gct gag tcc tgg aag cct gac gtt tgt acc 2657

Gly Asp Ile Phe Leu Ala Ala Glu Ser Trp Lys Pro Asp Val Cys Thr

600

605

610

615

agc tgc atc tgc att gat agc gta att agc tgt ttc tct gag tcc tgc 2705

Ser Cys Ile Cys Ile Asp Ser Val Ile Ser Cys Phe Ser Glu Ser Cys

620

625

630

cct tct gta tcc tgt gaa aga cct gtc ttg aga aaa ggc cag tgt tgt 2753

Pro Ser Val Ser Cys Glu Arg Pro Val Leu Arg Lys Gly Gln Cys Cys

635

640

645

ccc tac tgc ata gaa gac aca att cca aag aag gtg gtg tgc cac ttc 2801

Pro Tyr Cys Ile Glu Asp Thr Ile Pro Lys Lys Val Val Cys His Phe

650

655

660

agt ggg aag gcc tat gcc gac gag gag cgg tgg gac ctt gac agc tgc 2849

Ser Gly Lys Ala Tyr Ala Asp Glu Glu Arg Trp Asp Leu Asp Ser Cys

665

670

675

acc cac tac tac tgc ctg cag ggc cag acc ctc tgc tcg acc gtc agc 2897

Thr His Tyr Tyr Cys Leu Gln Gly Gln Thr Leu Cys Ser Thr Val Ser

680

685

690

695

tgc ccc cct ctg ccc tgt gtt gag ccc atc aac gtg gaa gga agt tgc 2945

Cys Pro Pro Leu Pro Cys Val Glu Pro Ile Asn Val Glu Gly Ser Cys

700

705

710

tgc cca atg tgt cca gtt tca cct tta cca tct ttg gat atg agt aca 2993

Cys Pro Met Cys Pro Val Ser Pro Leu Pro Ser Leu Asp Met Ser Thr

715

720

725

gaa cct atg agc tgt taggtgatta gcacctgtct ctttacagaa gaaactgagg 3048

Glu Pro Met Ser Cys

730

ctcaggaaaag agcccctgtg ggaagaggac tcactgtcat gcctcagctt ggtggagttt 3108

caccggaaat ctacccatat gcagggtcaa ggcaaaaagaa ttccaaagtt acgtctctcc 3168

ctctcactca ggaaaaaacc tgaggtggaa ctgaatcaat cccagctctg gggcctctgc 3228

agaaactttt actacttagc cattgacatt tacagtataa tacctatctg atcaaactgg 3288

ataatgtaaa tatatttact gaagatcagc ttctaataa aatggttcca gtggtaacat 3348

aatggacatc tga 3361

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<211> 732

<212> PRT

<213> Homo sapiens

<400> 20

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Ser Lys Ala Arg Cys Glu Val Gln Phe Ser Pro Arg Cys Pro Glu Asp

20 25 30

Ser Val Leu Ile Glu Gly Tyr Ala Pro Pro Gly Glu Cys Cys Pro Leu

35

40

45

Pro Ser Arg Cys Val Cys Asn Pro Ala Gly Cys Leu Arg Lys Val Cys

50

55

60

Gln Pro Gly Asn Leu Asn Ile Leu Val Ser Lys Ala Ser Gly Lys Pro

65

70

75

80

Gly Glu Cys Cys Asp Leu Tyr Glu Cys Lys Pro Val Phe Gly Val Asp

85

90

95

Cys Arg Thr Val Glu Cys Pro Pro Val Gln Gln Thr Ala Cys Pro Pro

100

105

110

Asp Ser Tyr Glu Thr Gln Val Arg Leu Thr Ala Asp Gly Cys Cys Thr

115

120

125

Leu Pro Thr Arg Cys Glu Cys Leu Ser Gly Leu Cys Gly Phe Pro Val

130

135

140

Cys Glu Val Gly Ser Thr Pro Arg Ile Val Ser Arg Gly Asp Gly Thr

145

150

155

160

Pro Gly Lys Cys Cys Asp Val Phe Glu Cys Val Asn Asp Thr Lys Pro

165

170

175

Ala Cys Val Phe Asn Asn Val Glu Tyr Tyr Asp Gly Asp Met Phe Arg

180

185

190

Met Asp Asn Cys Arg Phe Cys Arg Cys Gln Gly Gly Val Ala Ile Cys

195

200

205

Phe Thr Ala Gln Cys Gly Glu Ile Asn Cys Glu Arg Tyr Tyr Val Pro

210

215

220

Glu Gly Glu Cys Cys Pro Val Cys Glu Asp Pro Val Tyr Pro Phe Asn

225

230

235

240

Asn Pro Ala Gly Cys Tyr Ala Asn Gly Leu Ile Leu Ala His Gly Asp

245

250

255

Arg Trp Arg Glu Asp Asp Cys Thr Phe Cys Gln Cys Val Asn Gly Glu

260

265

270

Arg His Cys Val Ala Thr Val Cys Gly Gln Thr Cys Thr Asn Pro Val

275

280

285

Lys Val Pro Gly Glu Cys Cys Pro Val Cys Glu Glu Pro Thr Ile Ile

290

295

300

Thr Val Asp Pro Pro Ala Cys Gly Glu Leu Ser Asn Cys Thr Leu Thr

305

310

315

320

Gly Lys Asp Cys Ile Asn Gly Phe Lys Arg Asp His Asn Gly Cys Arg

325

330

335

Thr Cys Gln Cys Ile Asn Thr Glu Glu Leu Cys Ser Glu Arg Lys Gln

340

345

350

Gly Cys Thr Leu Asn Cys Pro Phe Gly Phe Leu Thr Asp Ala Gln Asn

355

360

365

Cys Glu Ile Cys Glu Cys Arg Pro Arg Pro Lys Lys Cys Arg Pro Ile

370

375

380

Ile Cys Asp Lys Tyr Cys Pro Leu Gly Leu Leu Lys Asn Lys His Gly

385

390

395

400

Cys Asp Ile Cys Arg Cys Lys Lys Cys Pro Glu Leu Ser Cys Ser Lys

405

410

415

Ile Cys Pro Leu Gly Phe Gln Gln Asp Ser Arg Gly Cys Leu Ile Cys

420

425

430

Lys Cys Arg Glu Ala Ser Ala Ser Ala Gly Pro Pro Ile Leu Ser Gly

435

440

445

Thr Cys Leu Thr Val Asp Gly His His His Lys Asn Glu Glu Ser Trp

450

455

460

His Asp Gly Cys Arg Glu Cys Tyr Cys Leu Asn Gly Arg Glu Met Cys

465

470

475

480

Ala Leu Ile Thr Cys Pro Val Pro Ala Cys Gly Asn Pro Thr Ile His

485

490

495

Pro Gly Gln Cys Cys Pro Ser Cys Ala Asp Asp Phe Val Val Gln Lys

500

505

510

Pro Glu Leu Ser Thr Pro Ser Ile Cys His Ala Pro Gly Gly Glu Tyr

515

520

525

Phe Val Glu Gly Glu Thr Trp Asn Ile Asp Ser Cys Thr Gln Cys Thr

530

535

540

Cys His Ser Gly Arg Val Leu Cys Glu Thr Glu Val Cys Pro Pro Leu

545 550 555 560

Leu Cys Gln Asn Pro Ser Arg Thr Gln Asp Ser Cys Cys Pro Gln Cys

565 570 575

Thr Asp Gln Pro Phe Arg Pro Ser Leu Ser Arg Asn Asn Ser Val Pro

580 585 590

Asn Tyr Cys Lys Asn Asp Glu Gly Asp Ile Phe Leu Ala Ala Glu Ser

595 600 605

Trp Lys Pro Asp Val Cys Thr Ser Cys Ile Cys Ile Asp Ser Val Ile

610 615 620

Ser Cys Phe Ser Glu Ser Cys Pro Ser Val Ser Cys Glu Arg Pro Val

625 630 635 640

Leu Arg Lys Gly Gln Cys Cys Pro Tyr Cys Ile Glu Asp Thr Ile Pro

645 650 655

Lys Lys Val Val Cys His Phe Ser Gly Lys Ala Tyr Ala Asp Glu Glu

660 665 670

Arg Trp Asp Leu Asp Ser Cys Thr His Tyr Tyr Cys Leu Gln Gly Gln

675

680

685

Thr Leu Cys Ser Thr Val Ser Cys Pro Pro Leu Pro Cys Val Glu Pro

690

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Ile Asn Val Glu Gly Ser Cys Cys Pro Met Cys Pro Val Ser Pro Leu

705

710

715

720

Pro Ser Leu Asp Met Ser Thr Glu Pro Met Ser Cys

725

730

<210> 21

<211> 1431

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (69)..(1211)

<220>

<221> variation

<222> (1)..(1431)

<223> where n can be any nucleotide

<400> 21

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agctagag atg ctg cac gct gct aac aag gga agg aag cct tca gct gag 110

Met Leu His Ala Ala Asn Lys Gly Arg Lys Pro Ser Ala Glu

1 5 10

gca ggt cgt ccc att cca cct aca tcc tcg cct agt ctc ctc cca tct 158

Ala Gly Arg Pro Ile Pro Pro Thr Ser Ser Pro Ser Leu Leu Pro Ser

15 20 25 30

gct cag ctg cct agc tcc cat aat cct cca cca gtt agc tgc cag atg 206

Ala Gln Leu Pro Ser Ser His Asn Pro Pro Pro Val Ser Cys Gln Met

35 40 45

cca ttg cta gac agc aac acc tcc cat caa atc atg gac acc aac cct 254

Pro Leu Leu Asp Ser Asn Thr Ser His Gln Ile Met Asp Thr Asn Pro

50 55 60

gat gag gaa ttc tcc ccc aat tca tac ctg ctc aga gca tgc tca ggg 302

Asp Glu Glu Phe Ser Pro Asn Ser Tyr Leu Leu Arg Ala Cys Ser Gly

65

70

75

ccc cag caa gcc tcc agc agt ggc cct ccg aac cac cac agc cag tcg 350

Pro Gln Gln Ala Ser Ser Ser Gly Pro Pro Asn His His Ser Gln Ser

80

85

90

act ctg agg ccc cct ctc cca ccc cct cac aac cac acg ctg tcc cat 398

Thr Leu Arg Pro Pro Leu Pro Pro Pro His Asn His Thr Leu Ser His

95

100

105

110

cac cac tcg tcc gcc aac tcc ctc aac agg aac tca ctg acc aat cgg 446

His His Ser Ser Ala Asn Ser Leu Asn Arg Asn Ser Leu Thr Asn Arg

115

120

125

cgg agt cag atc cac gcc ccg gcc cca gcg ccc aat gac ctg gcc acc 494

Arg Ser Gln Ile His Ala Pro Ala Pro Ala Pro Asn Asp Leu Ala Thr

130

135

140

aca cca gag tcc gtt cag ctt cag gac agc tgg gtg cta aac agc aac 542

Thr Pro Glu Ser Val Gln Leu Gln Asp Ser Trp Val Leu Asn Ser Asn

145

150

155

gtg cca ctg gag acc cgg cac ttc ctc ttc aag acc tcc tcg ggg agc 590

Val Pro Leu Glu Thr Arg His Phe Leu Phe Lys Thr Ser Ser Gly Ser

160

165

170

aca ccc ttg ttc agc agc tct tcc ccg gga tac cct ttg acc tca gga 638

Thr Pro Leu Phe Ser Ser Ser Ser Pro Gly Tyr Pro Leu Thr Ser Gly

175

180

185

190

acg gtt tac acg ccc ccg ccc cgc ctg ctg ccc agg aat act ttc tcc 686

Thr Val Tyr Thr Pro Pro Pro Arg Leu Leu Pro Arg Asn Thr Phe Ser

195

200

205

agg aag gct ttc aag ctg aag aag ccc tcc aaa tac tgc agc tgg aaa 734

Arg Lys Ala Phe Lys Leu Lys Lys Pro Ser Lys Tyr Cys Ser Trp Lys

210

215

220

tgt gct gcc ctc tcc gcc att gcc gcg gcc ctc ctc ttg gct att ttg 782

Cys Ala Ala Leu Ser Ala Ile Ala Ala Ala Leu Leu Leu Ala Ile Leu

225

230

235

ctg gcg tat ttc ata gtg ccc tgg tcg ttg aaa aac agc agc ata gac 830

Leu Ala Tyr Phe Ile Val Pro Trp Ser Leu Lys Asn Ser Ser Ile Asp

240

245

250

agt ggt gaa gca gaa gtt ggt cgg cgg gta aca caa gaa gtc cca cca 878

Ser Gly Glu Ala Glu Val Gly Arg Arg Val Thr Gln Glu Val Pro Pro

255 260 265 270

ggg gtg ttt tgg agg tca caa att cac atc agt cag ccc cag ttc tta 926

Gly Val Phe Trp Arg Ser Gln Ile His Ile Ser Gln Pro Gln Phe Leu

275 280 285

aag ttc aac atc tcc ctc ggg aag gac gct ctc ttt ggt gtt tac ata 974

Lys Phe Asn Ile Ser Leu Gly Lys Asp Ala Leu Phe Gly Val Tyr Ile

290 295 300

aga aga gga ctt cca cca tct cat gcc cag tat gac ttc atg gaa cgt 1022

Arg Arg Gly Leu Pro Pro Ser His Ala Gln Tyr Asp Phe Met Glu Arg

305 310 315

ctg gac ggg aag gag aag tgg agt gtg gtt gag tct ccc agg gaa cgc 1070

Leu Asp Gly Lys Glu Lys Trp Ser Val Val Glu Ser Pro Arg Glu Arg

320 325 330

cgg agc ata cag acc ttg gtt cag aat gaa gcc gtg ttt gtg cag tac 1118

Arg Ser Ile Gln Thr Leu Val Gln Asn Glu Ala Val Phe Val Gln Tyr

335 340 345 350

ctg gat gtg ggc ctg tgg cat ctg gcc ttc tac aat gat gga aaa gac 1166

Leu Asp Val Gly Leu Trp His Leu Ala Phe Tyr Asn Asp Gly Lys Asp

355

360

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aaa gag atg gtt tcc ttc aat act gtt gtc cta gat ggg acc atc 1211

Lys Glu Met Val Ser Phe Asn Thr Val Val Leu Asp Gly Thr Ile

370

375

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tagttgcaga aaaacaagct cagggcgccc actgatttga cattatgatt cagtgcagga 1271

ctgtccacgt aactgccatg ggaatggtga antgtgtgtc cggggtgtgt cactgtttcc 1331

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<211> 381

<212> PRT

<213> Homo sapiens

<400> 22

Met Leu His Ala Ala Asn Lys Gly Arg Lys Pro Ser Ala Glu Ala Gly

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Arg Pro Ile Pro Pro Thr Ser Ser Pro Ser Leu Leu Pro Ser Ala Gln

20

25

30

Leu Pro Ser Ser His Asn Pro Pro Pro Val Ser Cys Gln Met Pro Leu

35

40

45

Leu Asp Ser Asn Thr Ser His Gln Ile Met Asp Thr Asn Pro Asp Glu

50

55

60

Glu Phe Ser Pro Asn Ser Tyr Leu Leu Arg Ala Cys Ser Gly Pro Gln

65

70

75

80

Gln Ala Ser Ser Ser Gly Pro Pro Asn His His Ser Gln Ser Thr Leu

85

90

95

Arg Pro Pro Leu Pro Pro Pro His Asn His Thr Leu Ser His His His

100

105

110

Ser Ser Ala Asn Ser Leu Asn Arg Asn Ser Leu Thr Asn Arg Arg Ser

115

120

125

Gln Ile His Ala Pro Ala Pro Ala Pro Asn Asp Leu Ala Thr Thr Pro

130

135

140

Glu Ser Val Gln Leu Gln Asp Ser Trp Val Leu Asn Ser Asn Val Pro

145 150 155 160

Leu Glu Thr Arg His Phe Leu Phe Lys Thr Ser Ser Gly Ser Thr Pro

165 170 175

Leu Phe Ser Ser Ser Ser Pro Gly Tyr Pro Leu Thr Ser Gly Thr Val

180 185 190

Tyr Thr Pro Pro Pro Arg Leu Leu Pro Arg Asn Thr Phe Ser Arg Lys

195 200 205

Ala Phe Lys Leu Lys Lys Pro Ser Lys Tyr Cys Ser Trp Lys Cys Ala

210 215 220

Ala Leu Ser Ala Ile Ala Ala Ala Leu Leu Leu Ala Ile Leu Leu Ala

225 230 235 240

Tyr Phe Ile Val Pro Trp Ser Leu Lys Asn Ser Ser Ile Asp Ser Gly

245 250 255

Glu Ala Glu Val Gly Arg Arg Val Thr Gln Glu Val Pro Pro Gly Val

260 265 270

Phe Trp Arg Ser Gln Ile His Ile Ser Gln Pro Gln Phe Leu Lys Phe

275

280

285

Asn Ile Ser Leu Gly Lys Asp Ala Leu Phe Gly Val Tyr Ile Arg Arg

290

295

300

Gly Leu Pro Pro Ser His Ala Gln Tyr Asp Phe Met Glu Arg Leu Asp

305

310

315

320

Gly Lys Glu Lys Trp Ser Val Val Glu Ser Pro Arg Glu Arg Arg Ser

325

330

335

Ile Gln Thr Leu Val Gln Asn Glu Ala Val Phe Val Gln Tyr Leu Asp

340

345

350

Val Gly Leu Trp His Leu Ala Phe Tyr Asn Asp Gly Lys Asp Lys Glu

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Met Val Ser Phe Asn Thr Val Val Leu Asp Gly Thr Ile

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<400> 23

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cactccttgc agccctcgcc cgcaccttct ccaacacccc ggcatccctg caccacctgc 180

tcgggcagcc ccggcgggct ctgggacttg ctgtgcgcgc cgagaggaag gcaagctcca 240

aaccctgcc tggaagacgg gctgtcgcgg ctgcaccacc agcaggagga ggaggagaag 300

aaactatttc gcgatacccc attctgcggg tgctttgccg ctgccgttc tgctgccgcc 360

gatccgagtc cgcgggttcg aacaccgag cggtggggac ggtgggtccg gcgggcgcgc 420

ggaggaggac accagcggag ccctgcactc tcgtgccccg ctcaccagca tctacttgcc 480

ccctcgttcc ttccccagcc ctttagagaa gggacc atg att tgg aaa cgc agc 534

Met Ile Trp Lys Arg Ser

1

5

gcc gtt ctc cgc ttc tac agt gtc tgc ggg ctc ctg cta caa gcg gct 582

Ala Val Leu Arg Phe Tyr Ser Val Cys Gly Leu Leu Leu Gln Ala Ala

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15

20

gct tca aag aat aaa gtt aaa ggc agc caa ggg cag ttt cca cta aca 630

Ala Ser Lys Asn Lys Val Lys Gly Ser Gln Gly Gln Phe Pro Leu Thr

25

30

35

cag aat gta acc gtt gtt gaa ggt gga act gca att ttg acc tgc agg 678

Gln Asn Val Thr Val Val Glu Gly Gly Thr Ala Ile Leu Thr Cys Arg

40

45

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gtt gat caa aat gat aac acc tcc ctc cag tgg tca aat cca gct caa 726

Val Asp Gln Asn Asp Asn Thr Ser Leu Gln Trp Ser Asn Pro Ala Gln

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60

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cag act ctg tac ttt gac gac aag aaa gct tta agg gac aat agg atc 774

Gln Thr Leu Tyr Phe Asp Asp Lys Lys Ala Leu Arg Asp Asn Arg Ile

75

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gag ctg gtt cgc gct tcc tgg cat gaa ttg agt att agt gtc agt gat 822

Glu Leu Val Arg Ala Ser Trp His Glu Leu Ser Ile Ser Val Ser Asp

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gtg tct ctc tct gat gaa gga cag tac acc tgt tct tta ttt aca atg 870

Val Ser Leu Ser Asp Glu Gly Gln Tyr Thr Cys Ser Leu Phe Thr Met

105

110

115

cct gtc aaa act tcc aag gca tat ctc acc gtt ctg ggt gtt cct gaa 918

Pro Val Lys Thr Ser Lys Ala Tyr Leu Thr Val Leu Gly Val Pro Glu

120

125

130

aag cct cag att agt gga ttc tca tca cca gtt atg gag ggt gac ttg 966

Lys Pro Gln Ile Ser Gly Phe Ser Ser Pro Val Met Glu Gly Asp Leu

135

140

145

150

atg cag ctg act tgc aaa aca tct ggt agt aaa cct gca gct gat ata 1014

Met Gln Leu Thr Cys Lys Thr Ser Gly Ser Lys Pro Ala Ala Asp Ile

155

160

165

aga tgg ttc aaa aat gac aaa gag att aaa gat gta aaa tat tta aaa 1062

Arg Trp Phe Lys Asn Asp Lys Glu Ile Lys Asp Val Lys Tyr Leu Lys

170

175

180

gaa gag gat gca aat cgc aag aca ttc act gtc agc agc aca ctg gac 1110

Glu Glu Asp Ala Asn Arg Lys Thr Phe Thr Val Ser Ser Thr Leu Asp

185

190

195

ttc cga gtg gac cgg agt gat gat gga gtg gcg gtc atc tgc aga gta 1158

Phe Arg Val Asp Arg Ser Asp Asp Gly Val Ala Val Ile Cys Arg Val

200

205

210

gat cac gaa tcc ctc aat gcc acc cct cag gta gcc atg cag gtg cta 1206

Asp His Glu Ser Leu Asn Ala Thr Pro Gln Val Ala Met Gln Val Leu

215

220

225

230

gaa ata cac tat aca cca tca gtt aag att ata cca tcg act cct ttt 1254

Glu Ile His Tyr Thr Pro Ser Val Lys Ile Ile Pro Ser Thr Pro Phe

235

240

245

cca caa gaa gga cag cct tta att ttg act tgt gaa tcc aaa gga aaa 1302

Pro Gln Glu Gly Gln Pro Leu Ile Leu Thr Cys Glu Ser Lys Gly Lys

250

255

260

cca ctg cca gaa cct gtt ttg tgg aca aag gat ggc gga gaa tta cca 1350

Pro Leu Pro Glu Pro Val Leu Trp Thr Lys Asp Gly Gly Glu Leu Pro

265

270

275

gat cct gac cga atg gtt gtg agt ggt agg gag cta aac att ctt ttc 1398

Asp Pro Asp Arg Met Val Val Ser Gly Arg Glu Leu Asn Ile Leu Phe

280

285

290

ctg aac aaa acg gat aat ggt aca tat cga tgt gaa gcc aca aac acc 1446

Leu Asn Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Thr Asn Thr

295

300

305

310

att ggc caa agc agt gcg gaa tat gtt ctc att gtg cat gat cct aat 1494

Ile Gly Gln Ser Ser Ala Glu Tyr Val Leu Ile Val His Asp Pro Asn

315

320

325

gct ttg gct ggc cag aat ggc cct gac cat gct ctc ata gga gga ata 1542

Ala Leu Ala Gly Gln Asn Gly Pro Asp His Ala Leu Ile Gly Gly Ile

330

335

340

gtg gct gta gtt gta ttt gtc acg ctg tgt tct atc ttt ctg ctt ggt 1590

Val Ala Val Val Val Phe Val Thr Leu Cys Ser Ile Phe Leu Leu Gly

345

350

355

cga tat ctg gca agg cat aaa gga acg tat tta aca aat gaa gct aaa 1638

Arg Tyr Leu Ala Arg His Lys Gly Thr Tyr Leu Thr Asn Glu Ala Lys

360

365

370

gga gct gaa gat gca cca gat gct gat aca gcc att atc aat gct gaa 1686

Gly Ala Glu Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu

375

380

385

390

ggc agc caa gtc aat gct gaa gag aaa aaa gag tat ttc att 1728

Gly Ser Gln Val Asn Ala Glu Glu Lys Lys Glu Tyr Phe Ile

395

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taagatgcag gccagattc tgagttttac taccaggctg aatgctggag aaaactggct 1788

atcatctttc agaagtcatt tctaccatcg tctgctaccc ttattaactc ccatactgta 1848

ctgctatcag tagccagtgt ataccaacaa tcagctgttg aaagcatcat tctttaatta 1908

ctgtaccatc cataatgcag gacatttctt actgcctaaa ttccacacca ttgctctttt 1968

aacatacagt gcttgaatat acagccttaa caatgttaat catctccttg gatcattata 2028

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tttaagtcac agaccttacc agtttgcc 2116

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<212> PRT

<213> Homo sapiens

<400> 24

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Leu Leu Leu Gln Ala Ala Ala Ser Lys Asn Lys Val Lys Gly Ser Gln

20 25 30

Gly Gln Phe Pro Leu Thr Gln Asn Val Thr Val Val Glu Gly Gly Thr

35 40 45

Ala Ile Leu Thr Cys Arg Val Asp Gln Asn Asp Asn Thr Ser Leu Gln

50 55 60

Trp Ser Asn Pro Ala Gln Gln Thr Leu Tyr Phe Asp Asp Lys Lys Ala

65 70 75 80

Leu Arg Asp Asn Arg Ile Glu Leu Val Arg Ala Ser Trp His Glu Leu

85 90 95

Ser Ile Ser Val Ser Asp Val Ser Leu Ser Asp Glu Gly Gln Tyr Thr

100

105

110

Cys Ser Leu Phe Thr Met Pro Val Lys Thr Ser Lys Ala Tyr Leu Thr

115

120

125

Val Leu Gly Val Pro Glu Lys Pro Gln Ile Ser Gly Phe Ser Ser Pro

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140

Val Met Glu Gly Asp Leu Met Gln Leu Thr Cys Lys Thr Ser Gly Ser

145

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155

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Lys Pro Ala Ala Asp Ile Arg Trp Phe Lys Asn Asp Lys Glu Ile Lys

165

170

175

Asp Val Lys Tyr Leu Lys Glu Glu Asp Ala Asn Arg Lys Thr Phe Thr

180

185

190

Val Ser Ser Thr Leu Asp Phe Arg Val Asp Arg Ser Asp Asp Gly Val

195

200

205

Ala Val Ile Cys Arg Val Asp His Glu Ser Leu Asn Ala Thr Pro Gln

210

215

220

Val Ala Met Gln Val Leu Glu Ile His Tyr Thr Pro Ser Val Lys Ile

225 230 235 240

Ile Pro Ser Thr Pro Phe Pro Gln Glu Gly Gln Pro Leu Ile Leu Thr

245 250 255

Cys Glu Ser Lys Gly Lys Pro Leu Pro Glu Pro Val Leu Trp Thr Lys

260 265 270

Asp Gly Gly Glu Leu Pro Asp Pro Asp Arg Met Val Val Ser Gly Arg

275 280 285

Glu Leu Asn Ile Leu Phe Leu Asn Lys Thr Asp Asn Gly Thr Tyr Arg

290 295 300

Cys Glu Ala Thr Asn Thr Ile Gly Gln Ser Ser Ala Glu Tyr Val Leu

305 310 315 320

Ile Val His Asp Pro Asn Ala Leu Ala Gly Gln Asn Gly Pro Asp His

325 330 335

Ala Leu Ile Gly Gly Ile Val Ala Val Val Val Phe Val Thr Leu Cys

340 345 350

Ser Ile Phe Leu Leu Gly Arg Tyr Leu Ala Arg His Lys Gly Thr Tyr

355

360

365

Leu Thr Asn Glu Ala Lys Gly Ala Glu Asp Ala Pro Asp Ala Asp Thr

370

375

380

Ala Ile Ile Asn Ala Glu Gly Ser Gln Val Asn Ala Glu Glu Lys Lys

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395

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Glu Tyr Phe Ile

<210> 25

<211> 2862

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<213> Homo sapiens

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aggcagccac gttaagatgt ttttctgaca ataattggcc aagatattcc actgtgtctc 180

gaggccactc ctgaaaagag gaagtttgtt ttctgttgt tctgacagga agaggtggat 240

ctacttcac c aacatgcagt accaaattgt taggatacaa gctaaaaagg aggggattac 300

tcccagagga gggaaattgc tttacaatca ggcagttccc tttcaaagta tctcacctca 360

gaatgaaggg taacacttaa tcaacatgct atactgatct gggaacacag tttttattat 420

aaagctgagt tgtttattac attttagttt cattgagatt tacttgataa aggttgaaat 480

tggaacaaaa aaagccttca tcttaaa atg gtt ttt tcc act ttg ttg aat tgt 534

Met Val Phe Ser Thr Leu Leu Asn Cys

1

5

tcc tat act caa aat tgc acc aag aca cct tgt ctc cca aat gca aaa 582

Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys

10

15

20

25

tgt gaa ata cgc aat gga att gaa gcc tgc tat tgc aac atg gga ttt 630

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln

125

130

135

gaa gtc tat aga aat tct gtg aca gat ctt tca cca aca gat ata att 966

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile

140

145

150

gca tat ata gaa ata tta gct gaa tca tct tca tta cta ggt tac aag 1014

Ala Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys

155

160

165

aac aac act atc tca gcc aag gac acc ctt tct aac tca act ctt act 1062

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

170

175

180

185

gaa ttt gta aaa acc gtg aat aat ttt gtt caa agg gat aca ttt gta 1110

Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val

190

195

200

gtt tgg gac aag tta tct gtg aat cat agg aga aca cat ctt aca aaa 1158

Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys

205

210

215

ctc atg cac act gtt gaa caa gct act tta agg ata tcc cag agc ttc 1206

Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe
 220 225 230
 caa aag acc aca gag ttt gat aca aat tca acg gat ata gct ctc aaa 1254
 Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys
 235 240 245
 gtt ttc ttt ttt gat tca tat aac atg aaa cat att cat cct cat atg 1302
 Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met
 250 255 260 265
 aat atg gat gga gac tac ata aat ata ttt cca aag aga aaa gct gca 1350
 Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala
 270 275 280
 tat gat tca aat ggc aat gtt gca gtt gca ttt gta tat tat aag agt 1398
 Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Val Tyr Tyr Lys Ser
 285 290 295
 att ggt cct ttg ctt tca tca tct gac aac ttc tta ttg aaa cct caa 1446
 Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln
 300 305 310
 aat tat gat aat tct gaa gag gag gaa aga gtc ata tct tca gta att 1494

Asn Tyr Asp Asn Ser Glu Glu Glu Glu Arg Val Ile Ser Ser Val Ile

315

320

325

tca gtc tca atg agc tca aac cca ccc aca tta tat gaa ctt gaa aaa 1542

Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys

330

335

340

345

ata aca ttt aca tta agt cat cga aag gtc aca gat agg tat agg agt 1590

Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser

350

355

360

cta tgt gca ttt tgg aat tac tca cct gat acc atg aat ggc agc tgg 1638

Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp

365

370

375

tct tca gag ggc tgt gag ctg aca tac tca aat gag acc cac acc tca 1686

Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser

380

385

390

tgc cgc tgt aat cac ctg aca cat ttt gca att ttg atg tcc tct ggt 1734

Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly

395

400

405

cct tcc att ggt att aaa gat tat aat att ctt aca agg atc act caa 1782

Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln

410 415 420 425

cta gga ata att att tca ctg att tgt ctt gcc ata tgc att ttt acc 1830

Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr

430 435 440

ttc tgg ttc ttc agt gaa att caa agc acc agg aca aca att cac aaa 1878

Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys

445 450 455

aat ctt tgc tgt agc cta ttt ctt gct gaa ctt gtt ttt ctt gtt ggg 1926

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly

460 465 470

atc aat aca aat act aat aag ctc ttc tgt tca atc att gcc gga ctg 1974

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu

475 480 485

cta cac tac ttc ttt tta gct gct ttt gca tgg atg tgc att gaa ggc 2022

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly

490 495 500 505

ata cat ctc tat ctc att gtt gtg ggt gtc atc tac aac aag gga ttt 2070

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe

510

515

520

ttg cac aag aat ttt tat atc ttt ggc tat cta agc cca gcc gtg gta 2118

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val

525

530

535

gtt gga ttt tcg gca gca cta gga tac aga tat tat ggc aca acc aaa 2166

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys

540

545

550

gta tgt tgg ctt agc acc gaa aac aac ttt att tgg agt ttt ata gga 2214

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly

555

560

565

cca gca tgc cta atc att ctt gtt aat ctc ttg gct ttt gga gtc atc 2262

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile

570

575

580

585

ata tac aaa gtt ttt cgt cac act gca ggg ttg aaa cca gaa gtt agt 2310

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser

590

595

600

tgc ttt gag aac ata agg tct tgt gca aga gga gcc ctc gct ctt ctg 2358

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu

605

610

615

ttc ctt ctc ggc acc acc tgg atc ttt ggg gtt ctc cat gtt gtg cac 2406

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His

620

625

630

gca tca gtg gtt aca gct tac ctc ttc aca gtc agc aat gct ttc cag 2454

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln

635

640

645

ggg atg ttc att ttt tta ttc ctg tgt gtt tta tct aga aag att caa 2502

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln

650

655

660

665

gaa gaa tat tac aga ttg ttc aaa aat gtc ccc tgt tgt ttt gga tgt 2550

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys

670

675

680

tta agg taaacataga gaatggtgga taattacaac tgcacaaaaa taaaaattcc 2606

Leu Arg

aagctgtgga tgaccaatgt ataaaaatga ctcacaaat tatccaatta ttaactacta 2666

gacaaaaagt attttaaatc agtttttctg tttatgctat aggaactgta gataataagg 2726

taaaattatg tatcatatag atatactatg tttttctatg tgaaatagtt ctgtcaaaaa 2786

tagtattgca gatatttgga aagtaattgg tttctcagga gtgatatcac tgcaccaag 2846

gaaagatttt ctttct 2862

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<211> 683

<212> PRT

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<400> 26

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20 25 30

Glu Ala Cys Tyr Cys Asn Met Gly Phe Ser Gly Asn Gly Val Thr Ile

35 40 45

Cys Glu Asp Asp Asn Glu Cys Gly Asn Leu Thr Gln Ser Cys Gly Glu

50

55

60

Asn Ala Asn Cys Thr Asn Thr Glu Gly Ser Tyr Tyr Cys Met Cys Val

65

70

75

80

Pro Gly Phe Arg Ser Ser Ser Asn Gln Asp Arg Phe Ile Thr Asn Asp

85

90

95

Gly Thr Val Cys Ile Glu Asn Val Asn Ala Asn Cys His Leu Asp Asn

100

105

110

Val Cys Ile Ala Ala Asn Ile Asn Lys Thr Leu Thr Lys Ile Arg Ser

115

120

125

Ile Lys Glu Pro Val Ala Leu Leu Gln Glu Val Tyr Arg Asn Ser Val

130

135

140

Thr Asp Leu Ser Pro Thr Asp Ile Ile Ala Tyr Ile Glu Ile Leu Ala

145

150

155

160

Glu Ser Ser Ser Leu Leu Gly Tyr Lys Asn Asn Thr Ile Ser Ala Lys

165

170

175

Asp Thr Leu Ser Asn Ser Thr Leu Thr Glu Phe Val Lys Thr Val Asn

180

185

190

Asn Phe Val Gln Arg Asp Thr Phe Val Val Trp Asp Lys Leu Ser Val

195

200

205

Asn His Arg Arg Thr His Leu Thr Lys Leu Met His Thr Val Glu Gln

210

215

220

Ala Thr Leu Arg Ile Ser Gln Ser Phe Gln Lys Thr Thr Glu Phe Asp

225

230

235

240

Thr Asn Ser Thr Asp Ile Ala Leu Lys Val Phe Phe Phe Asp Ser Tyr

245

250

255

Asn Met Lys His Ile His Pro His Met Asn Met Asp Gly Asp Tyr Ile

260

265

270

Asn Ile Phe Pro Lys Arg Lys Ala Ala Tyr Asp Ser Asn Gly Asn Val

275

280

285

Ala Val Ala Phe Val Tyr Tyr Lys Ser Ile Gly Pro Leu Leu Ser Ser

290

295

300

Ser Asp Asn Phe Leu Leu Lys Pro Gln Asn Tyr Asp Asn Ser Glu Glu

305 310 315 320

Glu Glu Arg Val Ile Ser Ser Val Ile Ser Val Ser Met Ser Ser Asn

325 330 335

Pro Pro Thr Leu Tyr Glu Leu Glu Lys Ile Thr Phe Thr Leu Ser His

340 345 350

Arg Lys Val Thr Asp Arg Tyr Arg Ser Leu Cys Ala Phe Trp Asn Tyr

355 360 365

Ser Pro Asp Thr Met Asn Gly Ser Trp Ser Ser Glu Gly Cys Glu Leu

370 375 380

Thr Tyr Ser Asn Glu Thr His Thr Ser Cys Arg Cys Asn His Leu Thr

385 390 395 400

His Phe Ala Ile Leu Met Ser Ser Gly Pro Ser Ile Gly Ile Lys Asp

405 410 415

Tyr Asn Ile Leu Thr Arg Ile Thr Gln Leu Gly Ile Ile Ile Ser Leu

420 425 430

Ile Cys Leu Ala Ile Cys Ile Phe Thr Phe Trp Phe Phe Ser Glu Ile

435

440

445

Gln Ser Thr Arg Thr Thr Ile His Lys Asn Leu Cys Cys Ser Leu Phe

450

455

460

Leu Ala Glu Leu Val Phe Leu Val Gly Ile Asn Thr Asn Thr Asn Lys

465

470

475

480

Leu Phe Cys Ser Ile Ile Ala Gly Leu Leu His Tyr Phe Phe Leu Ala

485

490

495

Ala Phe Ala Trp Met Cys Ile Glu Gly Ile His Leu Tyr Leu Ile Val

500

505

510

Val Gly Val Ile Tyr Asn Lys Gly Phe Leu His Lys Asn Phe Tyr Ile

515

520

525

Phe Gly Tyr Leu Ser Pro Ala Val Val Val Gly Phe Ser Ala Ala Leu

530

535

540

Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys Val Cys Trp Leu Ser Thr Glu

545

550

555

560

Asn Asn Phe Ile Trp Ser Phe Ile Gly Pro Ala Cys Leu Ile Ile Leu

565

570

575

Val Asn Leu Leu Ala Phe Gly Val Ile Ile Tyr Lys Val Phe Arg His

580

585

590

Thr Ala Gly Leu Lys Pro Glu Val Ser Cys Phe Glu Asn Ile Arg Ser

595

600

605

Cys Ala Arg Gly Ala Leu Ala Leu Leu Phe Leu Leu Gly Thr Thr Trp

610

615

620

Ile Phe Gly Val Leu His Val Val His Ala Ser Val Val Thr Ala Tyr

625

630

635

640

Leu Phe Thr Val Ser Asn Ala Phe Gln Gly Met Phe Ile Phe Leu Phe

645

650

655

Leu Cys Val Leu Ser Arg Lys Ile Gln Glu Glu Tyr Tyr Arg Leu Phe

660

665

670

Lys Asn Val Pro Cys Cys Phe Gly Cys Leu Arg

675

680

<210> 27

<211> 2760

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (520) .. (2454)

<400> 27

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tagggctcga gcggctgccc gggcaggta catttgtttg cctgattccc agctctctta 120

ggataggtct tcttgggaaa tgctttcatt tctaatacaa agaaaattgt gcaggcagcc 180

acgttaagat gtttttctga caataattgg ccaagatatt ccactgtgtc tcgaggccac 240

tcttgaaaag aggaagtttg ttttcctgtt gttctgacag gaagaggtgg atctacttca 300

tcaacatgca gtaccaaatt gttaggatac aagctaaaaa ggagggcatc cttccttgaa 360

tgtggggtag gaacctttcc gaagtgggga tcttatgacc tacaagtggt tttttccact 420

ttgttgaatt gttcctatac tcaaaattgc accaagacac cttgtctccc aaatgcaaaa 480

tgtgaaatac gcaatggaat tgaagcctgc tattgcaac atg gga ttt tca gga 534

Met Gly Phe Ser Gly

1 5

aat ggt gtc aca att tgt gaa gat gat aat gaa tgt gga aat tta act 582

Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn Leu Thr

10 15 20

cag tcc tgt ggc gaa aat gct aat tgc act aac aca gaa gga agt tat 630

Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly Ser Tyr

25 30 35

tat tgt atg tgt gta cct ggc ttc aga tcc agc agt aac caa gac agg 678

Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln Asp Arg

40 45 50

ttt atc act aat gat gga acc gtc tgt ata gaa aat gtg aat gca aac 726

Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn Ala Asn

55 60 65

tgc cat tta gat aat gtc tgt ata gct gca aat att aat aaa act tta 774

Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys Thr Leu

70 75 80 85

aca aaa atc aga tcc ata aaa gaa cct gtg gct ttg cta caa gaa gtc 822

Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln Glu Val

90 95 100

tat aga aat tct gtg aca gat ctt tca cca aca gat ata att gca tat 870

Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile Ala Tyr

105 110 115

ata gaa ata tta gct gaa tca tct tca tta cta ggt tac aag aac aac 918

Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys Asn Asn

120 125 130

act atc tca gcc aag gac acc ctt tct aac tca act ctt act gaa ttt 966

Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr Glu Phe

135 140 145

gta aaa acc gtg aat aat ttt gtt caa agg gat aca ttt gta gtt tgg 1014

Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val Val Trp

150 155 160 165

gac aag tta tct gtg aat cat agg aga aca cat ctt aca aaa ctc atg 1062

Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys Leu Met

170

175

180

cac act gtt gaa caa gct act tta agg ata tcc cag agc ttc caa aag 1110

His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe Gln Lys

185

190

195

acc aca gag ttt gat aca aat tca acg gat ata gct ctc aaa gtt ttc 1158

Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys Val Phe

200

205

210

ttt ttt gat tca tat aac atg aaa cat att cat cct cat atg aat atg 1206

Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met Asn Met

215

220

225

gat gga gac tac ata aat ata ttt cca aag aga aaa gct gca tat gat 1254

Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala Tyr Asp

230

235

240

245

tca aat ggc aat gtt gca gtt gca ttt gta tat tat aag agt att ggt 1302

Ser Asn Gly Asn Val Ala Val Ala Phe Val Tyr Tyr Lys Ser Ile Gly

250

255

260

cct ttg ctt tca tca tct gac aac ttc tta ttg aaa cct caa aat tat 1350

Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly Pro Ser

360

365

370

att ggt att aaa gat tat aat att ctt aca agg atc act caa cta gga 1686

Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln Leu Gly

375

380

385

ata att att tca ctg att tgt ctt gcc ata tgc att ttt acc ttc tgg 1734

Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr Phe Trp

390

395

400

405

ttc ttc agt gaa att caa agc acc agg aca aca att cac aaa aat ctt 1782

Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys Asn Leu

410

415

420

tgc tgt agc cta ttt ctt gct gaa ctt gtt ttt ctt gtt ggg atc aat 1830

Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly Ile Asn

425

430

435

aca aat act aat aag ctc ttc tgt tca atc att gcc gga ctg cta cac 1878

Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu Leu His

440

445

450

tac ttc ttt tta gct gct ttt gca tgg atg tgc att gaa ggc ata cat 1926

Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly Ile His

455

460

465

ctc tat ctc att gtt gtg ggt gtc atc tac aac aag gga ttt ttg cac 1974

Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe Leu His

470

475

480

485

aag aat ttt tat atc ttt ggc tat cta agc cca gcc gtg gta gtt gga 2022

Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val Val Gly

490

495

500

ttt tcg gca gca cta gga tac aga tat tat ggc aca acc aaa gta tgt 2070

Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys Val Cys

505

510

515

tgg ctt agc acc gaa aac aac ttt att tgg agt ttt ata gga cca gca 2118

Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly Pro Ala

520

525

530

tgc cta atc att ctt gtt aat ctc ttg gct ttt gga gtc atc ata tac 2166

Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile Ile Tyr

535

540

545

aaa gtt ttt cgt cac act gca ggg ttg aaa cca gaa gtt agt tgc ttt 2214

Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser Cys Phe

550 555 560 565

gag aac ata agg tct tgt gca aga gga gcc ctc gct ctt ctg ttc ctt 2262

Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu Phe Leu

570 575 580

ctc ggc acc acc tgg atc ttt ggg gtt ctc cat gtt gtg cac gca tca 2310

Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His Ala Ser

585 590 595

gtg gtt aca gct tac ctc ttc aca gtc agc aat gct ttc cag ggg atg 2358

Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln Gly Met

600 605 610

ttc att ttt tta ttc ctg tgt gtt tta tct aga aag att caa gaa gaa 2406

Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln Glu Glu

615 620 625

tat tac aga ttg ttc aaa aat gtc ccc tgt tgt ttt gga tgt tta agg 2454

Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys Leu Arg

630 635 640 645

taaacataga gaatggtgga taattacaac tgcacaaaaa taaaaattcc aagctgtgga 2514

tgaccaatgt ataaaaatga ctcatcaaat tatccaatta ttaactacta gacaaaaagt 2574

atTTTaaatc agTTTTtctg tttatgctat aggaactgta gataataagg taaaattatg 2634

tatcatatag atatactatg tttttctatg tgaaatagtt ctgtcaaaaa tagtattgca 2694

gatatttgga aagtaattgg tttctcagga gtgatatcac tgcacccaag gaaagatttt 2754

ctttct 2760

<210> 28

<211> 645

<212> PRT

<213> Homo sapiens

<400> 28

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1 5 10 15

Cys Gly Asn Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn

20 25 30

Thr Glu Gly Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser

35

40

45

Ser Asn Gln Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu

50

55

60

Asn Val Asn Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn

65

70

75

80

Ile Asn Lys Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala

85

90

95

Leu Leu Gln Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr

100

105

110

Asp Ile Ile Ala Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu

115

120

125

Gly Tyr Lys Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser

130

135

140

Thr Leu Thr Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp

145

150

155

160

Thr Phe Val Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His

165

170

175

Leu Thr Lys Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser

180

185

190

Gln Ser Phe Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile

195

200

205

Ala Leu Lys Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His

210

215

220

Pro His Met Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg

225

230

235

240

Lys Ala Ala Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Val Tyr

245

250

255

Tyr Lys Ser Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu

260

265

270

Lys Pro Gln Asn Tyr Asp Asn Ser Glu Glu Glu Glu Arg Val Ile Ser

275

280

285

Ser Val Ile Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu

290

295

300

Leu Glu Lys Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg

305

310

315

320

Tyr Arg Ser Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn

325

330

335

Gly Ser Trp Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr

340

345

350

His Thr Ser Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met

355

360

365

Ser Ser Gly Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg

370

375

380

Ile Thr Gln Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys

385

390

395

400

Ile Phe Thr Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr

405

410

415

Ile His Lys Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe

420

425

430

Leu Val Gly Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile

435

440

445

Ala Gly Leu Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys

450

455

460

Ile Glu Gly Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn

465

470

475

480

Lys Gly Phe Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro

485

490

495

Ala Val Val Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly

500

505

510

Thr Thr Lys Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser

515

520

525

Phe Ile Gly Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe

530

535

540

Gly Val Ile Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro

545 550 555 560

Glu Val Ser Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu

565 570 575

Ala Leu Leu Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His

580 585 590

Val Val His Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn

595 600 605

Ala Phe Gln Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg

610 615 620

Lys Ile Gln Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys

625 630 635 640

Phe Gly Cys Leu Arg

645

<210> 29

<211> 727

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (312)..(560)

<220>

<221> variation

<222> (1)..(727)

<223> where n can be any nucleotide

<400> 29

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caagtctctg atataaaatg acccagtaca gtcaaccttg catatctgca gatacagaac 120

ccactgactg tgttttcaca gaatagctta ttgtaagttt tctagaactg aacctggatg 180

tgcattctggc acagtgtgat gctggattct gtgtcctcat tagtctaacg agtctactct 240

gttgcccaca tcacctccca ttaggaccac tatgcccttt taaaaagtgg tctttataag 300

atgtaagtat t atg aca ccc ttc ntg cat aca act att caa tgg ctt ttg 350

Met Thr Pro Phe Xaa His Thr Thr Ile Gln Trp Leu Leu

1 5 10

att agc ctt agg ata aaa atc ccg tcc tgc cgc acc gac ttg tcc atc 398

Ile Ser Leu Arg Ile Lys Ile Pro Ser Cys Arg Thr Asp Leu Ser Ile

15 20 25

ttg tgg gta gcc act tgt tac tac ctc tct cag tgt cct tcc cag aca 446

Leu Trp Val Ala Thr Cys Tyr Tyr Leu Ser Gln Cys Pro Ser Gln Thr

30 35 40 45

tgc tgc ttc cac tcc tct ccc ctc aga tcc ccg ttt tgc tta gtt act 494

Cys Cys Phe His Ser Ser Pro Leu Arg Ser Pro Phe Cys Leu Val Thr

50 55 60

tcc tcc tca tct ttc agg tct caa agt agt tgt ccc ttc act gaa tgc 542

Ser Ser Ser Ser Phe Arg Ser Gln Ser Ser Cys Pro Phe Thr Glu Cys

65 70 75

acc gac aac ctg gcc cag taaagttact ttgtcgtctg cgcccaaata 590

Thr Asp Asn Leu Ala Gln

80

atcctaccct tccatctgct acattcctta aatctgcaat cccttggtca aagcctgcaa 650

aagagcatga gctccttgaa gcaaagacag tattagtcac ttttaatgta aagtataaaa 710

aaaaaaaaaa aaaaaaa

727

<210> 30

<211> 83

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)..(83)

<223> where Xaa can any amino acid

<400> 30

Met Thr Pro Phe Xaa His Thr Thr Ile Gln Trp Leu Leu Ile Ser Leu

1

5

10

15

Arg Ile Lys Ile Pro Ser Cys Arg Thr Asp Leu Ser Ile Leu Trp Val

20

25

30

Ala Thr Cys Tyr Tyr Leu Ser Gln Cys Pro Ser Gln Thr Cys Cys Phe

35

40

45

His Ser Ser Pro Leu Arg Ser Pro Phe Cys Leu Val Thr Ser Ser Ser

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Ser Phe Arg Ser Gln Ser Ser Cys Pro Phe Thr Glu Cys Thr Asp Asn

65

70

75

80

Leu Ala Gln

<210> 31

<211> 2741

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (288) .. (2021)

<400> 31

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tagttttttt cttggagaaa gtctgacatg tgaggcacag atgagttatt aaaggcagat 120

gactttccag ccttgtctta aatgttccat tctttacctt agaaattatt taaatttgtg 180

tctgtccca gagcatccgc aagggcgcag ccagtggtt tggagtcagc ggcgactggg 240

aggggcagcg gcagcagtgg cagcgccgca gcctgcacca ctgcagc atg cgc tac 296

Met Arg Tyr

1

ggc cgc ctg aag gcc tcg tgc cag cgt gac ctg gag ctc ccc agc cag 344

Gly Arg Leu Lys Ala Ser Cys Gln Arg Asp Leu Glu Leu Pro Ser Gln

5

10

15

gag gca ccg tcc ttc cag ggc act gag tcc cca aag ccc tgc aag atg 392

Glu Ala Pro Ser Phe Gln Gly Thr Glu Ser Pro Lys Pro Cys Lys Met

20

25

30

35

ccc aag att gtg gat ccg ctg gcc cgg ggc cgg gcc ttc cgc cac ccg 440

Pro Lys Ile Val Asp Pro Leu Ala Arg Gly Arg Ala Phe Arg His Pro

40

45

50

gag gag atg gac agg ccc cac gcc ctg cac cca ccg ctg acc ccc gga 488

Glu Glu Met Asp Arg Pro His Ala Leu His Pro Pro Leu Thr Pro Gly

55

60

65

gtc ctg tcc ctc acc tcc ttc acc agt gtc cgt tct ggc tac tcc cac 536

Val Leu Ser Leu Thr Ser Phe Thr Ser Val Arg Ser Gly Tyr Ser His

70

75

80

ctg cca cgc cgc aag aga atg tct gtg gcc cac atg agc ttg caa gct 584

Leu Pro Arg Arg Lys Arg Met Ser Val Ala His Met Ser Leu Gln Ala

85

90

95

gcc gct gcc ctc ctc aag ggg cgc tcg gtg ctg gat gcc acc gga cag 632

Ala Ala Ala Leu Leu Lys Gly Arg Ser Val Leu Asp Ala Thr Gly Gln

100

105

110

115

cgg tgc cgg gtg gtc aag cgc agc ttt gcc ttc ccg agc ttc ctg gag 680

Arg Cys Arg Val Val Lys Arg Ser Phe Ala Phe Pro Ser Phe Leu Glu

120

125

130

gag gat gtg gtc gat ggg gca gac acg ttt gac tcc tcc ttt ttt agt 728

Glu Asp Val Val Asp Gly Ala Asp Thr Phe Asp Ser Ser Phe Phe Ser

135

140

145

aag gaa gaa atg agc tcc atg cct gat gat gtc ttt gag tcc ccc cca 776

Lys Glu Glu Met Ser Ser Met Pro Asp Asp Val Phe Glu Ser Pro Pro

150	155	160	
ctc tct gcc agc tac ttc cga ggg atc cca cac tca gcc tcc cct gtc			824
Leu Ser Ala Ser Tyr Phe Arg Gly Ile Pro His Ser Ala Ser Pro Val			
165	170	175	
tcc ccc gat ggg gtg caa atc cct ctg aag gag tat ggc cga gcc cca			872
Ser Pro Asp Gly Val Gln Ile Pro Leu Lys Glu Tyr Gly Arg Ala Pro			
180	185	190	195
gtc ccc ggg ccc cgg cgc ggc aag cgc atc gcc tcc aag gtg aag cac			920
Val Pro Gly Pro Arg Arg Gly Lys Arg Ile Ala Ser Lys Val Lys His			
200	205	210	
ttt gcc ttt gat cgg aag aag cgg cac tac ggc ctc ggc gtg gtg ggc			968
Phe Ala Phe Asp Arg Lys Lys Arg His Tyr Gly Leu Gly Val Val Gly			
215	220	225	
aac tgg ctg aac cgc agc tac cgc cgc agc atc agc agc act gtg cag			1016
Asn Trp Leu Asn Arg Ser Tyr Arg Arg Ser Ile Ser Ser Thr Val Gln			
230	235	240	
cgg cag ctg gag agc ttc gac agc cac cgg ccc tac ttc acc tac tgg			1064
Arg Gln Leu Glu Ser Phe Asp Ser His Arg Pro Tyr Phe Thr Tyr Trp			

245	250	255	
ctg acc ttc gtc cat gtc atc atc acg ctg ctg gtg att tgc acg tat 1112			
Leu Thr Phe Val His Val Ile Ile Thr Leu Leu Val Ile Cys Thr Tyr			
260	265	270	275
ggc atc gca ccc gtg ggc ttt gcc cag cac gtc acc acc cag ctg gtg 1160			
Gly Ile Ala Pro Val Gly Phe Ala Gln His Val Thr Thr Gln Leu Val			
	280	285	290
ctg cgg aac aaa ggt gtg tac gag agc gtg aag tac atc cag cag gag 1208			
Leu Arg Asn Lys Gly Val Tyr Glu Ser Val Lys Tyr Ile Gln Gln Glu			
	295	300	305
aac ttc tgg gtt ggc ccc agc tcg att gac ctg atc cac ctg ggg gcc 1256			
Asn Phe Trp Val Gly Pro Ser Ser Ile Asp Leu Ile His Leu Gly Ala			
	310	315	320
aag ttc tca ccc tgc atc cgg aag gac ggg cag atc gag cag ctg gtg 1304			
Lys Phe Ser Pro Cys Ile Arg Lys Asp Gly Gln Ile Glu Gln Leu Val			
	325	330	335
ctg cgc gag cga gac ctg gag cgg gac tca ggc tgc tgt gtc cag aat 1352			
Leu Arg Glu Arg Asp Leu Glu Arg Asp Ser Gly Cys Cys Val Gln Asn			

340	345	350	355	
gac cac tcc ggc tgc atc cag acc cag cgg aag gac tgc tcg gag act				1400
Asp His Ser Gly Cys Ile Gln Thr Gln Arg Lys Asp Cys Ser Glu Thr				
	360	365	370	
ttg gcc act ttt gtc aag tgg cag gat gac act ggg ccc ccc atg gac				1448
Leu Ala Thr Phe Val Lys Trp Gln Asp Asp Thr Gly Pro Pro Met Asp				
	375	380	385	
aag tct gat ctg ggc cag aag cgg act tcg ggg gct gtc tgc cac cag				1496
Lys Ser Asp Leu Gly Gln Lys Arg Thr Ser Gly Ala Val Cys His Gln				
	390	395	400	
gac ccc agg acc tgc gag gag cca gcc tcc agc ggt gcc cac atc tgg				1544
Asp Pro Arg Thr Cys Glu Glu Pro Ala Ser Ser Gly Ala His Ile Trp				
	405	410	415	
ccc gat gac atc act aag tgg ccg atc tgc aca gag cag gcc agg agc				1592
Pro Asp Asp Ile Thr Lys Trp Pro Ile Cys Thr Glu Gln Ala Arg Ser				
420	425	430	435	
aac cac aca ggc ttc ctg cac atg gac tgc gag atc aag ggc cgc ccc				1640
Asn His Thr Gly Phe Leu His Met Asp Cys Glu Ile Lys Gly Arg Pro				

440

445

450

tgc tgc atc ggc acc aag ggc agc tgt gag atc acc acc cgg gaa tac 1688

Cys Cys Ile Gly Thr Lys Gly Ser Cys Glu Ile Thr Thr Arg Glu Tyr

455

460

465

tgt gag ttc atg cac ggc tat ttc cat gag gaa gca aca ctc tgc tcc 1736

Cys Glu Phe Met His Gly Tyr Phe His Glu Glu Ala Thr Leu Cys Ser

470

475

480

cag gtg agg cga ggc agg cct gga gta gtg gag gag agg acg ctg ggc 1784

Gln Val Arg Arg Gly Arg Pro Gly Val Val Glu Glu Arg Thr Leu Gly

485

490

495

atg gca gcc tgc tgg ggc cgg ggc tca cgc act ccc tcc cat gtc gga 1832

Met Ala Ala Cys Trp Gly Arg Gly Ser Arg Thr Pro Ser His Val Gly

500

505

510

515

gcc tca gac tca gcc tgc ttc tgg ggc gct gag cac cat atg ccc act 1880

Ala Ser Asp Ser Ala Cys Phe Trp Gly Ala Glu His His Met Pro Thr

520

525

530

ccc agg tgc act gct tgg aca agg tgt gtg ggc tgc tgc cct tcc tca 1928

Pro Arg Cys Thr Ala Trp Thr Arg Cys Val Gly Cys Cys Pro Ser Ser

535

540

545

acc ctg agg tcc cag atc agt tct aca ggc tct ggc tgt ctc tct tcc 1976

Thr Leu Arg Ser Gln Ile Ser Ser Thr Gly Ser Gly Cys Leu Ser Ser

550

555

560

tac atg ctg gcg tgg tgc act gcc tcg tgt ctg tgg tct ttc aaa 2021

Tyr Met Leu Ala Trp Cys Thr Ala Ser Cys Leu Trp Ser Phe Lys

565

570

575

tgaccatcct gagggacctg gagaagctgg ccggctggca ccgtatcgcc atcatcttca 2081

tcttcagtgg catcacaggc aacctcgcca gtgccatctt tctcccatat cgggcagagg 2141

tgggcccggc eggctcacag ttcggcctcc tcgcctgcct ctctgtggag ctcttccaga 2201

gctggccgct gctggagagg ccctggaagg ccttctcaa cctctcgacc atcgtgctct 2261

tctgttcat ctgtggcttc ctgccttga tcgacaacat cgcacacatc ttgggcttcc 2321

tcagtggcct gctgctggcc ttgccttcc tgccctacat caccttcggc accagcgaca 2381

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gcttcccctt caccagccgc ttctgcgaga agtatgagct ggaccaggtg ctgcactgac 2561

cgctgggcca cacggctgcc cctcagccct gctggaacag ggtctgcctg cgagggctgc 2621

cctctgcaga gcgctctctg tgtgccagag agccagagac ccaagacagg gcccgggctc 2681

tggacctggg tgccccctg ccaggcgagg ctgactccgc gtgagatggg tggttaaggc 2741

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<211> 578

<212> PRT

<213> Homo sapiens

<400> 32

Met Arg Tyr Gly Arg Leu Lys Ala Ser Cys Gln Arg Asp Leu Glu Leu

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Pro Ser Gln Glu Ala Pro Ser Phe Gln Gly Thr Glu Ser Pro Lys Pro

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Cys Lys Met Pro Lys Ile Val Asp Pro Leu Ala Arg Gly Arg Ala Phe

35

40

45

Arg His Pro Glu Glu Met Asp Arg Pro His Ala Leu His Pro Pro Leu

50

55

60

Thr Pro Gly Val Leu Ser Leu Thr Ser Phe Thr Ser Val Arg Ser Gly

65

70

75

80

Tyr Ser His Leu Pro Arg Arg Lys Arg Met Ser Val Ala His Met Ser

85

90

95

Leu Gln Ala Ala Ala Ala Leu Leu Lys Gly Arg Ser Val Leu Asp Ala

100

105

110

Thr Gly Gln Arg Cys Arg Val Val Lys Arg Ser Phe Ala Phe Pro Ser

115

120

125

Phe Leu Glu Glu Asp Val Val Asp Gly Ala Asp Thr Phe Asp Ser Ser

130

135

140

Phe Phe Ser Lys Glu Glu Met Ser Ser Met Pro Asp Asp Val Phe Glu

145

150

155

160

Ser Pro Pro Leu Ser Ala Ser Tyr Phe Arg Gly Ile Pro His Ser Ala

	165	170	175
Ser Pro Val Ser Pro Asp Gly Val Gln Ile Pro Leu Lys Glu Tyr Gly			
	180	185	190
Arg Ala Pro Val Pro Gly Pro Arg Arg Gly Lys Arg Ile Ala Ser Lys			
	195	200	205
Val Lys His Phe Ala Phe Asp Arg Lys Lys Arg His Tyr Gly Leu Gly			
	210	215	220
Val Val Gly Asn Trp Leu Asn Arg Ser Tyr Arg Arg Ser Ile Ser Ser			
225	230	235	240
Thr Val Gln Arg Gln Leu Glu Ser Phe Asp Ser His Arg Pro Tyr Phe			
	245	250	255
Thr Tyr Trp Leu Thr Phe Val His Val Ile Ile Thr Leu Leu Val Ile			
	260	265	270
Cys Thr Tyr Gly Ile Ala Pro Val Gly Phe Ala Gln His Val Thr Thr			
	275	280	285
Gln Leu Val Leu Arg Asn Lys Gly Val Tyr Glu Ser Val Lys Tyr Ile			

290	295	300	
Gln Gln Glu Asn Phe Trp Val Gly Pro Ser Ser Ile Asp Leu Ile His			
305	310	315	320
Leu Gly Ala Lys Phe Ser Pro Cys Ile Arg Lys Asp Gly Gln Ile Glu			
	325	330	335
Gln Leu Val Leu Arg Glu Arg Asp Leu Glu Arg Asp Ser Gly Cys Cys			
	340	345	350
Val Gln Asn Asp His Ser Gly Cys Ile Gln Thr Gln Arg Lys Asp Cys			
	355	360	365
Ser Glu Thr Leu Ala Thr Phe Val Lys Trp Gln Asp Asp Thr Gly Pro			
	370	375	380
Pro Met Asp Lys Ser Asp Leu Gly Gln Lys Arg Thr Ser Gly Ala Val			
385	390	395	400
Cys His Gln Asp Pro Arg Thr Cys Glu Glu Pro Ala Ser Ser Gly Ala			
	405	410	415
His Ile Trp Pro Asp Asp Ile Thr Lys Trp Pro Ile Cys Thr Glu Gln			

420	425	430	
Ala Arg Ser Asn His Thr Gly Phe Leu His Met Asp Cys Glu Ile Lys			
435	440	445	
Gly Arg Pro Cys Cys Ile Gly Thr Lys Gly Ser Cys Glu Ile Thr Thr			
450	455	460	
Arg Glu Tyr Cys Glu Phe Met His Gly Tyr Phe His Glu Glu Ala Thr			
465	470	475	480
Leu Cys Ser Gln Val Arg Arg Gly Arg Pro Gly Val Val Glu Glu Arg			
485	490	495	
Thr Leu Gly Met Ala Ala Cys Trp Gly Arg Gly Ser Arg Thr Pro Ser			
500	505	510	
His Val Gly Ala Ser Asp Ser Ala Cys Phe Trp Gly Ala Glu His His			
515	520	525	
Met Pro Thr Pro Arg Cys Thr Ala Trp Thr Arg Cys Val Gly Cys Cys			
530	535	540	
Pro Ser Ser Thr Leu Arg Ser Gln Ile Ser Ser Thr Gly Ser Gly Cys			

545 550 555 560

Leu Ser Ser Tyr Met Leu Ala Trp Cys Thr Ala Ser Cys Leu Trp Ser

565 570 575

Phe Lys

<210> 33

<211> 2596

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (289)..(2412)

<400> 33

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tgactttcca gccttgctct aaatgttcca ttctttacct tagaaattat ttaaatttgt 180

gtcctgtccc agagcatccg caagggcgca gcccagtggg ttggagtcag cggcgactgg 240

gaggggcagc ggcagcagtg gcagcgccgc agcctgcacc actgcagc atg cgc tac 297

Met Arg Tyr

1

ggc cgc ctg aag gcc tcg tgc cag cgt gac ctg gag ctc ccc agc cag 345

Gly Arg Leu Lys Ala Ser Cys Gln Arg Asp Leu Glu Leu Pro Ser Gln

5

10

15

gag gca ccg tcc ttc cag ggc act gag tcc cca aag ccc tgc aag atg 393

Glu Ala Pro Ser Phe Gln Gly Thr Glu Ser Pro Lys Pro Cys Lys Met

20

25

30

35

ccc aag att gtg gat ccg ctg gcc cgg ggc cgg gcc ttc cgc cac ccg 441

Pro Lys Ile Val Asp Pro Leu Ala Arg Gly Arg Ala Phe Arg His Pro

40

45

50

gag gag atg gac agg ccc cac gcc ctg cac cca ccg ctg acc ccc gga 489

Glu Glu Met Asp Arg Pro His Ala Leu His Pro Pro Leu Thr Pro Gly

55

60

65

gtc ctg tcc ctc acc tcc ttc acc agt gtc cgt tct ggc tac tcc cac 537

Val Leu Ser Leu Thr Ser Phe Thr Ser Val Arg Ser Gly Tyr Ser His

70

75

80

ctg cca cgc cgc aag aga atg tct gtg gcc cac atg agc ttg caa gct 585

Leu Pro Arg Arg Lys Arg Met Ser Val Ala His Met Ser Leu Gln Ala

85

90

95

gcc gct gcc ctc ctc aag ggg cgc tcg gtg ctg gat gcc acc gga cag 633

Ala Ala Ala Leu Leu Lys Gly Arg Ser Val Leu Asp Ala Thr Gly Gln

100

105

110

115

cgg tgc cgg gtg gtc aag cgc agc ttt gcc ttc ccg agc ttc ctg gag 681

Arg Cys Arg Val Val Lys Arg Ser Phe Ala Phe Pro Ser Phe Leu Glu

120

125

130

gag gat gtg gtc gat ggg gca gac acg ttt gac tcc tcc ttt ttt agt 729

Glu Asp Val Val Asp Gly Ala Asp Thr Phe Asp Ser Ser Phe Phe Ser

135

140

145

aag gaa gaa atg agc tcc atg cct gat gat gtc ttt gag tcc ccc cca 777

Lys Glu Glu Met Ser Ser Met Pro Asp Asp Val Phe Glu Ser Pro Pro

150

155

160

ctc tct gcc agc tac ttc cga ggg atc cca cac tca gcc tcc cct gtc 825

Leu Ser Ala Ser Tyr Phe Arg Gly Ile Pro His Ser Ala Ser Pro Val

165

170

175

tcc ccc gat ggg gtg caa atc cct ctg aag gag tat ggc cga gcc cca 873

Ser Pro Asp Gly Val Gln Ile Pro Leu Lys Glu Tyr Gly Arg Ala Pro

180

185

190

195

gtc ccc ggg ccc cgg cgc ggc aag cgc atc gcc tcc aag gtg aag cac 921

Val Pro Gly Pro Arg Arg Gly Lys Arg Ile Ala Ser Lys Val Lys His

200

205

210

ttt gcc ttt gat cgg aag aag cgg cac tac ggc ctc ggc gtg gtg ggc 969

Phe Ala Phe Asp Arg Lys Lys Arg His Tyr Gly Leu Gly Val Val Gly

215

220

225

aac tgg ctg aac cgc agc tac cgc cgc agc atc agc agc act gtg cag 1017

Asn Trp Leu Asn Arg Ser Tyr Arg Arg Ser Ile Ser Ser Thr Val Gln

230

235

240

cgg cag ctg gag agc ttc gac agc cac cgg ccc tac ttc acc tac tgg 1065

Arg Gln Leu Glu Ser Phe Asp Ser His Arg Pro Tyr Phe Thr Tyr Trp

245

250

255

ctg acc ttc gtc cat gtc atc atc acg ctg ctg gtg att tgc acg tat 1113

Leu Thr Phe Val His Val Ile Ile Thr Leu Leu Val Ile Cys Thr Tyr	
260	265 270 275
ggc atc gca ccc gtg ggc ttt gcc cag cac gtc acc acc cag ctg gtg	1161
Gly Ile Ala Pro Val Gly Phe Ala Gln His Val Thr Thr Gln Leu Val	
280	285 290
ctg cgg aac aaa ggt gtg tac gag agc gtg aag tac atc cag cag gag	1209
Leu Arg Asn Lys Gly Val Tyr Glu Ser Val Lys Tyr Ile Gln Gln Glu	
295	300 305
aac ttc tgg gtt ggc ccc agc tcg att gac ctg atc cac ctg ggg gcc	1257
Asn Phe Trp Val Gly Pro Ser Ser Ile Asp Leu Ile His Leu Gly Ala	
310	315 320
aag ttc tca ccc tgc atc cgg aag gac ggg cag atc gag cag ctg gtg	1305
Lys Phe Ser Pro Cys Ile Arg Lys Asp Gly Gln Ile Glu Gln Leu Val	
325	330 335
ctg cgc gag cga gac ctg gag cgg gac tca ggc tgc tgt gtc cag aat	1353
Leu Arg Glu Arg Asp Leu Glu Arg Asp Ser Gly Cys Cys Val Gln Asn	
340	345 350 355
gac cac tcc ggc tgc atc cag acc cag cgg aag gac tgc tcg gag act	1401

Asp His Ser Gly Cys Ile Gln Thr Gln Arg Lys Asp Cys Ser Glu Thr

360

365

370

ttg gcc act ttt gtc aag tgg cag gat gac act ggg ccc ccc atg gac 1449

Leu Ala Thr Phe Val Lys Trp Gln Asp Asp Thr Gly Pro Pro Met Asp

375

380

385

aag tct gat ctg ggc cag aag cgg act tcg ggg gct gtc tgc cac cag 1497

Lys Ser Asp Leu Gly Gln Lys Arg Thr Ser Gly Ala Val Cys His Gln

390

395

400

gac ccc agg acc tgc gag gag cca gcc tcc agc ggt gcc cac atc tgg 1545

Asp Pro Arg Thr Cys Glu Glu Pro Ala Ser Ser Gly Ala His Ile Trp

405

410

415

ccc gat gac atc act aag tgg ccg atc tgc aca gag cag gcc agg agc 1593

Pro Asp Asp Ile Thr Lys Trp Pro Ile Cys Thr Glu Gln Ala Arg Ser

420

425

430

435

aac cac aca ggc ttc ctg cac atg gac tgc gag atc aag ggc cgc ccc 1641

Asn His Thr Gly Phe Leu His Met Asp Cys Glu Ile Lys Gly Arg Pro

440

445

450

tgc tgc atc ggc acc aag ggc agc tgt gag atc acc acc cgg gaa tac 1689

Cys Cys Ile Gly Thr Lys Gly Ser Cys Glu Ile Thr Thr Arg Glu Tyr

455

460

465

tgt gag ttc atg cac ggc tat ttc cat gag gaa gca aca ctc tgc tcc 1737

Cys Glu Phe Met His Gly Tyr Phe His Glu Glu Ala Thr Leu Cys Ser

470

475

480

cag gtg cac tgc ttg gac aag gtg tgt ggg ctg ctg ccc ttc ctc aac 1785

Gln Val His Cys Leu Asp Lys Val Cys Gly Leu Leu Pro Phe Leu Asn

485

490

495

cct gag gtc cca gat cag ttc tac agg ctc tgg ctg tct ctc ttc cta 1833

Pro Glu Val Pro Asp Gln Phe Tyr Arg Leu Trp Leu Ser Leu Phe Leu

500

505

510

515

cat gct ggc gtg gtg cac tgc ctc gtg tct gtg gtc ttt caa atg acc 1881

His Ala Gly Val Val His Cys Leu Val Ser Val Val Phe Gln Met Thr

520

525

530

atc ctg agg gac ctg gag aag ctg gcc ggc tgg cac cgt atc gcc atc 1929

Ile Leu Arg Asp Leu Glu Lys Leu Ala Gly Trp His Arg Ile Ala Ile

535

540

545

atc ttc atc ctc agt ggc atc aca ggc aac ctc gcc agt acc atc ttt 1977

Ile Phe Ile Leu Ser Gly Ile Thr Gly Asn Leu Ala Ser Thr Ile Phe

550

555

560

ctc cca tac cgg gca gag gtg ggc ccg gcc ggc tca cag ttc ggc ctc 2025

Leu Pro Tyr Arg Ala Glu Val Gly Pro Ala Gly Ser Gln Phe Gly Leu

565

570

575

ctc gcc tgc ctc ttc gtg gag ctc ttc cag agc tgg ccg ctg ctg gag 2073

Leu Ala Cys Leu Phe Val Glu Leu Phe Gln Ser Trp Pro Leu Leu Glu

580

585

590

595

agg ccc tgg aag gcc ttc ctc aac ctc tcg acc atc gtg ctc ttc ctg 2121

Arg Pro Trp Lys Ala Phe Leu Asn Leu Ser Thr Ile Val Leu Phe Leu

600

605

610

ttc atc tgt ggc ctc ctg ccc tgg atc gac aac atc gcc cac atc ttc 2169

Phe Ile Cys Gly Leu Leu Pro Trp Ile Asp Asn Ile Ala His Ile Phe

615

620

625

ggc ttc ctc agt ggc ctg ctg ctg gcc ttc gcc ttc ctg ccc tac atc 2217

Gly Phe Leu Ser Gly Leu Leu Leu Ala Phe Ala Phe Leu Pro Tyr Ile

630

635

640

acc ttc ggc acc agc gac aag tac cgc aag cgg gca ctc atc ctg gtg 2265

Thr Phe Gly Thr Ser Asp Lys Tyr Arg Lys Arg Ala Leu Ile Leu Val

645

650

655

tca ctg ctg gcc ttt gcc ggc ctc ttc gcc gcc ctc gtg ctg tgg ctg 2313

Ser Leu Leu Ala Phe Ala Gly Leu Phe Ala Ala Leu Val Leu Trp Leu

660

665

670

675

tac atc tac ccc att aac tgg ccc tgg atc gag cac ctc acc tgc ttc 2361

Tyr Ile Tyr Pro Ile Asn Trp Pro Trp Ile Glu His Leu Thr Cys Phe

680

685

690

ccc ttc acc agc cgc ttc tgc gag aag tat gag ctg gac cag gtg ctg 2409

Pro Phe Thr Ser Arg Phe Cys Glu Lys Tyr Glu Leu Asp Gln Val Leu

695

700

705

cac tgaccgctgg gccacacggc tgcccctcag ccctgctgga acagggctctg 2462

His

cctgcgaggg ctgccctctg cagagcgctc tctgtgtgcc agagagccag agaccaaga 2522

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tggttggtta aggc

2596

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<211> 708

<212> PRT

<213> Homo sapiens

<400> 34

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Pro Ser Gln Glu Ala Pro Ser Phe Gln Gly Thr Glu Ser Pro Lys Pro

20 25 30

Cys Lys Met Pro Lys Ile Val Asp Pro Leu Ala Arg Gly Arg Ala Phe

35 40 45

Arg His Pro Glu Glu Met Asp Arg Pro His Ala Leu His Pro Pro Leu

50 55 60

Thr Pro Gly Val Leu Ser Leu Thr Ser Phe Thr Ser Val Arg Ser Gly

65 70 75 80

Tyr Ser His Leu Pro Arg Arg Lys Arg Met Ser Val Ala His Met Ser

85 90 95

Leu Gln Ala Ala Ala Ala Leu Leu Lys Gly Arg Ser Val Leu Asp Ala

100

105

110

Thr Gly Gln Arg Cys Arg Val Val Lys Arg Ser Phe Ala Phe Pro Ser

115

120

125

Phe Leu Glu Glu Asp Val Val Asp Gly Ala Asp Thr Phe Asp Ser Ser

130

135

140

Phe Phe Ser Lys Glu Glu Met Ser Ser Met Pro Asp Asp Val Phe Glu

145

150

155

160

Ser Pro Pro Leu Ser Ala Ser Tyr Phe Arg Gly Ile Pro His Ser Ala

165

170

175

Ser Pro Val Ser Pro Asp Gly Val Gln Ile Pro Leu Lys Glu Tyr Gly

180

185

190

Arg Ala Pro Val Pro Gly Pro Arg Arg Gly Lys Arg Ile Ala Ser Lys

195

200

205

Val Lys His Phe Ala Phe Asp Arg Lys Lys Arg His Tyr Gly Leu Gly

210

215

220

Val Val Gly Asn Trp Leu Asn Arg Ser Tyr Arg Arg Ser Ile Ser Ser

225 230 235 240

Thr Val Gln Arg Gln Leu Glu Ser Phe Asp Ser His Arg Pro Tyr Phe

245 250 255

Thr Tyr Trp Leu Thr Phe Val His Val Ile Ile Thr Leu Leu Val Ile

260 265 270

Cys Thr Tyr Gly Ile Ala Pro Val Gly Phe Ala Gln His Val Thr Thr

275 280 285

Gln Leu Val Leu Arg Asn Lys Gly Val Tyr Glu Ser Val Lys Tyr Ile

290 295 300

Gln Gln Glu Asn Phe Trp Val Gly Pro Ser Ser Ile Asp Leu Ile His

305 310 315 320

Leu Gly Ala Lys Phe Ser Pro Cys Ile Arg Lys Asp Gly Gln Ile Glu

325 330 335

Gln Leu Val Leu Arg Glu Arg Asp Leu Glu Arg Asp Ser Gly Cys Cys

340 345 350

Val Gln Asn Asp His Ser Gly Cys Ile Gln Thr Gln Arg Lys Asp Cys

355

360

365

Ser Glu Thr Leu Ala Thr Phe Val Lys Trp Gln Asp Asp Thr Gly Pro

370

375

380

Pro Met Asp Lys Ser Asp Leu Gly Gln Lys Arg Thr Ser Gly Ala Val

385

390

395

400

Cys His Gln Asp Pro Arg Thr Cys Glu Glu Pro Ala Ser Ser Gly Ala

405

410

415

His Ile Trp Pro Asp Asp Ile Thr Lys Trp Pro Ile Cys Thr Glu Gln

420

425

430

Ala Arg Ser Asn His Thr Gly Phe Leu His Met Asp Cys Glu Ile Lys

435

440

445

Gly Arg Pro Cys Cys Ile Gly Thr Lys Gly Ser Cys Glu Ile Thr Thr

450

455

460

Arg Glu Tyr Cys Glu Phe Met His Gly Tyr Phe His Glu Glu Ala Thr

465

470

475

480

Leu Cys Ser Gln Val His Cys Leu Asp Lys Val Cys Gly Leu Leu Pro

485

490

495

Phe Leu Asn Pro Glu Val Pro Asp Gln Phe Tyr Arg Leu Trp Leu Ser

500

505

510

Leu Phe Leu His Ala Gly Val Val His Cys Leu Val Ser Val Val Phe

515

520

525

Gln Met Thr Ile Leu Arg Asp Leu Glu Lys Leu Ala Gly Trp His Arg

530

535

540

Ile Ala Ile Ile Phe Ile Leu Ser Gly Ile Thr Gly Asn Leu Ala Ser

545

550

555

560

Thr Ile Phe Leu Pro Tyr Arg Ala Glu Val Gly Pro Ala Gly Ser Gln

565

570

575

Phe Gly Leu Leu Ala Cys Leu Phe Val Glu Leu Phe Gln Ser Trp Pro

580

585

590

Leu Leu Glu Arg Pro Trp Lys Ala Phe Leu Asn Leu Ser Thr Ile Val

595

600

605

Leu Phe Leu Phe Ile Cys Gly Leu Leu Pro Trp Ile Asp Asn Ile Ala

610

615

620

His Ile Phe Gly Phe Leu Ser Gly Leu Leu Leu Ala Phe Ala Phe Leu

625

630

635

640

Pro Tyr Ile Thr Phe Gly Thr Ser Asp Lys Tyr Arg Lys Arg Ala Leu

645

650

655

Ile Leu Val Ser Leu Leu Ala Phe Ala Gly Leu Phe Ala Ala Leu Val

660

665

670

Leu Trp Leu Tyr Ile Tyr Pro Ile Asn Trp Pro Trp Ile Glu His Leu

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695

700

Gln Val Leu His

705

<210> 35

<211> 705

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (135)..(545)

<400> 35

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atacactagt gatc atg ttc agc cct gct tcc acc tgc ata gaa tct ttt 170

Met Phe Ser Pro Ala Ser Thr Cys Ile Glu Ser Phe

1

5

10

ctt ctc aga cag gga cag tgc agc ctc aac atc tcc tgg agt cta gaa 218

Leu Leu Arg Gln Gly Gln Cys Ser Leu Asn Ile Ser Trp Ser Leu Glu

15

20

25

gct gtt tcc ttt ccc ctc ctt cct cct ctt gct cta gcc tta ata ctg 266

Ala Val Ser Phe Pro Leu Leu Pro Pro Leu Ala Leu Ala Leu Ile Leu

30

35

40

gcc ttt tcc ctc cct gcc cca agt gaa gac agg gca ctc tgc gcc cac 314

Ala Phe Ser Leu Pro Ala Pro Ser Glu Asp Arg Ala Leu Cys Ala His

45 50 55 60

cac atg cac agc tgt gca tgg aga cct gca ggt gca cgt gct gga aca 362

His Met His Ser Cys Ala Trp Arg Pro Ala Gly Ala Arg Ala Gly Thr

65 70 75

cgt gtg gtt ccc ccc tgg ccc agc ctc ctc tgc agt gcc cct ctc ccc 410

Arg Val Val Pro Pro Trp Pro Ser Leu Leu Cys Ser Ala Pro Leu Pro

80 85 90

tgc cca tcc tcc cca cgg aag cat gtg ctg gtc aca ctg gtt ctc cag 458

Cys Pro Ser Ser Pro Arg Lys His Val Leu Val Thr Leu Val Leu Gln

95 100 105

ggg tct gtg atg ggg ccc ctg ggg gtc agc ttc tgt ccc tct gcc ttc 506

Gly Ser Val Met Gly Pro Leu Gly Val Ser Phe Cys Pro Ser Ala Phe

110 115 120

tca cct ctt tgt tcc ttt ctt ttc atg tat cca ttc agt tgatgtttat 555

Ser Pro Leu Cys Ser Phe Leu Phe Met Tyr Pro Phe Ser

125 130 135

tgagcaacta cagatgtcag cactgtgtta ggtgctgggg gccctgcgtg ggaagataaa 615

gttcctccct caaggactcc ccatccagct gggagacaga caactaacta cactgcaccc 675

tgcggtttgc aaggggctcc tgcctggctc 705

<210> 36

<211> 137

<212> PRT

<213> Homo sapiens

<400> 36

Met Phe Ser Pro Ala Ser Thr Cys Ile Glu Ser Phe Leu Leu Arg Gln

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Gly Gln Cys Ser Leu Asn Ile Ser Trp Ser Leu Glu Ala Val Ser Phe

20 25 30

Pro Leu Leu Pro Pro Leu Ala Leu Ala Leu Ile Leu Ala Phe Ser Leu

35 40 45

Pro Ala Pro Ser Glu Asp Arg Ala Leu Cys Ala His His Met His Ser

50	55	60
Cys Ala Trp Arg Pro Ala Gly Ala Arg Ala Gly Thr Arg Val Val Pro		
65	70	75
Pro Trp Pro Ser Leu Leu Cys Ser Ala Pro Leu Pro Cys Pro Ser Ser		
85	90	95
Pro Arg Lys His Val Leu Val Thr Leu Val Leu Gln Gly Ser Val Met		
100	105	110
Gly Pro Leu Gly Val Ser Phe Cys Pro Ser Ala Phe Ser Pro Leu Cys		
115	120	125
Ser Phe Leu Phe Met Tyr Pro Phe Ser		
130	135	

<210> 37

<211> 1149

<212> DNA

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<220>

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<222> (389) .. (856)

<400> 37

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ctccttcttc tctgcccctc cccatgggtc tctagggggc tgggtgcaggc agcagcagag 180

gcactctggg cagctgggtg agggcccatc tgggcaaggc cccagcgcc tgccttctct 240

cccggggccc tgtgggcaag cctcctgctt cactttcagg tttctcgaag tgccttcttg 300

ctcctgtctg tttcccatc ctgccagatt tctgtttctc ttgctgggct tttggcagta 360

gggggctgtg ttggtgggcc ctacgaag atg ctc agt gct cga gat cgc cgg 412

Met Leu Ser Ala Arg Asp Arg Arg

1

5

gac cgg cac cct gag gag ggg gta gtt gca gag ctc cag ggc ttc gcg 460

Asp Arg His Pro Glu Glu Gly Val Val Ala Glu Leu Gln Gly Phe Ala

10

15

20

gtg gac aag gcc ttc ctc acc tcc cac aag ggc atc ctg ctg gaa acc 508

Val Asp Lys Ala Phe Leu Thr Ser His Lys Gly Ile Leu Leu Glu Thr

25 30 35 40

gag ctg gcc ctg acc ctc atc atc ttc atc tgc ttc acg gcc tcc atc 556

Glu Leu Ala Leu Thr Leu Ile Ile Phe Ile Cys Phe Thr Ala Ser Ile

45 50 55

tct gcc tac atg gcc gcg gcg cta ctg gag ttc ttc atc aca ctt gcc 604

Ser Ala Tyr Met Ala Ala Ala Leu Leu Glu Phe Phe Ile Thr Leu Ala

60 65 70

ttc ctc ttc ctc tat gcc acc cag tac tac cag cgc ttc gac cga att 652

Phe Leu Phe Leu Tyr Ala Thr Gln Tyr Tyr Gln Arg Phe Asp Arg Ile

75 80 85

aac tgg ccc tgt ctg gac ttc ctg cgc tgt gtc agt gcc atc atc atc 700

Asn Trp Pro Cys Leu Asp Phe Leu Arg Cys Val Ser Ala Ile Ile Ile

90 95 100

ttc ctg gtg gtc tcc ttt gca gct gtg acc tcc cgg gac gga gct gcc 748

Phe Leu Val Val Ser Phe Ala Ala Val Thr Ser Arg Asp Gly Ala Ala

105 110 115 120

att gct gct ttt gtt ttt ggc atc atc ctg gtt tcc atc ttt gcc tat 796

Ile Ala Ala Phe Val Phe Gly Ile Ile Leu Val Ser Ile Phe Ala Tyr

125

130

135

gat gcc ttc aag atc tac cgg act gag atg gca ccc ggg gcc agc cag 844

Asp Ala Phe Lys Ile Tyr Arg Thr Glu Met Ala Pro Gly Ala Ser Gln

140

145

150

ggg gac cag cag tgactctggg gctacctggc tcctaggccc agccagccag 896

Gly Asp Gln Gln

155

agaggacagt ggagcccaga cacgtctcct tgggattcac tagccccag ccgcgcaaac 956

cccaccccaa ccctacacag cagtctggcc tgagacgtca ctggggactt atctgtggag 1016

cctggtgctc caggatgtgg cttctcatga agctctggcc agaggagggg aacttattgg 1076

ggggggggggg tggaggggag gaatctggac ctctaagtca ttcccaaatt aaaatattca 1136

aattcttaaa aaa

1149

<210> 38

<211> 156

<212> PRT

<213> Homo sapiens

<400> 38

Met Leu Ser Ala Arg Asp Arg Arg Asp Arg His Pro Glu Glu Gly Val

1 5 10 15

Val Ala Glu Leu Gln Gly Phe Ala Val Asp Lys Ala Phe Leu Thr Ser

20 25 30

His Lys Gly Ile Leu Leu Glu Thr Glu Leu Ala Leu Thr Leu Ile Ile

35 40 45

Phe Ile Cys Phe Thr Ala Ser Ile Ser Ala Tyr Met Ala Ala Ala Leu

50 55 60

Leu Glu Phe Phe Ile Thr Leu Ala Phe Leu Phe Leu Tyr Ala Thr Gln

65 70 75 80

Tyr Tyr Gln Arg Phe Asp Arg Ile Asn Trp Pro Cys Leu Asp Phe Leu

85 90 95

Arg Cys Val Ser Ala Ile Ile Ile Phe Leu Val Val Ser Phe Ala Ala

100

105

110

Val Thr Ser Arg Asp Gly Ala Ala Ile Ala Ala Phe Val Phe Gly Ile

115

120

125

Ile Leu Val Ser Ile Phe Ala Tyr Asp Ala Phe Lys Ile Tyr Arg Thr

130

135

140

Glu Met Ala Pro Gly Ala Ser Gln Gly Asp Gln Gln

145

150

155

<210> 39

<211> 1611

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (505)..(1284)

<400> 39

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aagctcgatc cccaaagaaa agagcgagtg ggcaggcagc tgcgagacag aaccggagtg 120

tgcaggggtcc ctagaggccg gttcctggtc tgtgctgctc tcctggaagc catggtacag 180

gcagagctca gggcgatccc caggtgaggg cagcggctct gcctgggatt ccaccgcagt 240

acaaccgggt agatgcgggg tggagaagaa aggatgttgc ctgcactgct cgccaatagc 300

accctgagag gctacatttg cagaagcagc agcagcagaa gacacagcgc cgggccagga 360

ggcggctcga gctgttcgta aagtcgcccg acagcttttt ctccgtagta tgcgagttga 420

caaaacagcc agagaacagg gtcccccatt acaatctttt cgagatcttt tcccttgcta 480

accggatctg atttgtgcga aaac atg cct tgc act tgt acc tgg agg aac 531

Met Pro Cys Thr Cys Thr Trp Arg Asn

1

5

tgg aga cag tgg att cga cct tta gta gcg gtc atc tac ctg gtg tca 579

Trp Arg Gln Trp Ile Arg Pro Leu Val Ala Val Ile Tyr Leu Val Ser

10

15

20

25

ata gtg gtt gcg gtt ccc cta tgc gtg tgg gaa tta cag aaa ctg gag 627

Ile Val Val Ala Val Pro Leu Cys Val Trp Glu Leu Gln Lys Leu Glu

30

35

40

gtt gga ata cac acc aag gct tgg ttt att gct gga atc ttt ttg ctg 675

Val Gly Ile His Thr Lys Ala Trp Phe Ile Ala Gly Ile Phe Leu Leu

45

50

55

ttg act att cct ata tca ctg tgg gtg ata ttg caa cac tta gtg cat 723

Leu Thr Ile Pro Ile Ser Leu Trp Val Ile Leu Gln His Leu Val His

60

65

70

tat aca caa cct gaa cta caa aaa cca ata ata agg att ctt tgg atg 771

Tyr Thr Gln Pro Glu Leu Gln Lys Pro Ile Ile Arg Ile Leu Trp Met

75

80

85

gta cct att tac agt tta gat agt tgg ata gct ttg aaa tat ccc gga 819

Val Pro Ile Tyr Ser Leu Asp Ser Trp Ile Ala Leu Lys Tyr Pro Gly

90

95

100

105

att gca ata tat gtg gat acc tgc aga gaa tgc tat gaa gct tat gta 867

Ile Ala Ile Tyr Val Asp Thr Cys Arg Glu Cys Tyr Glu Ala Tyr Val

110

115

120

att tac aac ttt atg gga ttc ctt acc aat tat cta act aac cgg tat 915

Ile Tyr Asn Phe Met Gly Phe Leu Thr Asn Tyr Leu Thr Asn Arg Tyr

125	130	135	
cca aat ctg gta tta atc ctt gaa gcc aaa gat caa cag aaa cat ttc 963			
Pro Asn Leu Val Leu Ile Leu Glu Ala Lys Asp Gln Gln Lys His Phe			
140	145	150	
cct cct tta tgt tgc tgt cca cca tgg gct atg gga gaa gta ttg ctg 1011			
Pro Pro Leu Cys Cys Cys Pro Pro Trp Ala Met Gly Glu Val Leu Leu			
155	160	165	
ttt agg tgc aaa cta ggt gta tta cag tac aca gtt gtc aga cct ttc 1059			
Phe Arg Cys Lys Leu Gly Val Leu Gln Tyr Thr Val Val Arg Pro Phe			
170	175	180	185
acc acc atc gtt gct tta atc tgt gag ctg ctt ggt ata tat gac gaa 1107			
Thr Thr Ile Val Ala Leu Ile Cys Glu Leu Leu Gly Ile Tyr Asp Glu			
190	195	200	
ggg aac ttt agc ttt tca aat gct tgg act tat ttg gtt ata ata aac 1155			
Gly Asn Phe Ser Phe Ser Asn Ala Trp Thr Tyr Leu Val Ile Ile Asn			
205	210	215	
aac atg tca cag ttg ttt gcc atg tat tgt ctc ctg ctc ttt tat aaa 1203			
Asn Met Ser Gln Leu Phe Ala Met Tyr Cys Leu Leu Leu Phe Tyr Lys			

220

225

230

gta cta aaa gaa gaa ctg agc cca atc caa cct gtt ggc aaa ttt ctt 1251

Val Leu Lys Glu Glu Leu Ser Pro Ile Gln Pro Val Gly Lys Phe Leu

235

240

245

tgt gta aag ctg gtg gtt ttt gtt tct ttt tgg taagtgttac ttttttttaa 1304

Cys Val Lys Leu Val Val Phe Val Ser Phe Trp

250

255

260

atgttctcat tttttaagg gcagtaaaaa ccgttgatta aggaggattt ttaaacagtc 1364

ttaatgcgga agatagatta aaatgtctct acttctcttt ttaaaagtgc atcttttttag 1424

cccttctaca attttcaaaa gaaataatta gatggtcgct gtaacattta tatgaagaaa 1484

atagtttgag acaacctaaa tatgtcaata ctagaataat tattaaaata aatcatggcc 1544

ctgtcatata atagaatact atggagtttg gaagaaagca tgatgtagaa tatttaatta 1604

tatggga

1611

<210> 40

<211> 260

<212> PRT

<213> Homo sapiens

<400> 40

Met Pro Cys Thr Cys Thr Trp Arg Asn Trp Arg Gln Trp Ile Arg Pro

1 5 10 15

Leu Val Ala Val Ile Tyr Leu Val Ser Ile Val Val Ala Val Pro Leu

20 25 30

Cys Val Trp Glu Leu Gln Lys Leu Glu Val Gly Ile His Thr Lys Ala

35 40 45

Trp Phe Ile Ala Gly Ile Phe Leu Leu Leu Thr Ile Pro Ile Ser Leu

50 55 60

Trp Val Ile Leu Gln His Leu Val His Tyr Thr Gln Pro Glu Leu Gln

65 70 75 80

Lys Pro Ile Ile Arg Ile Leu Trp Met Val Pro Ile Tyr Ser Leu Asp

85 90 95

Ser Trp Ile Ala Leu Lys Tyr Pro Gly Ile Ala Ile Tyr Val Asp Thr

100	105	110	
Cys Arg Glu Cys Tyr Glu Ala Tyr Val Ile Tyr Asn Phe Met Gly Phe			
115	120	125	
Leu Thr Asn Tyr Leu Thr Asn Arg Tyr Pro Asn Leu Val Leu Ile Leu			
130	135	140	
Glu Ala Lys Asp Gln Gln Lys His Phe Pro Pro Leu Cys Cys Cys Pro			
145	150	155	160
Pro Trp Ala Met Gly Glu Val Leu Leu Phe Arg Cys Lys Leu Gly Val			
165	170	175	
Leu Gln Tyr Thr Val Val Arg Pro Phe Thr Thr Ile Val Ala Leu Ile			
180	185	190	
Cys Glu Leu Leu Gly Ile Tyr Asp Glu Gly Asn Phe Ser Phe Ser Asn			
195	200	205	
Ala Trp Thr Tyr Leu Val Ile Ile Asn Asn Met Ser Gln Leu Phe Ala			
210	215	220	
Met Tyr Cys Leu Leu Leu Phe Tyr Lys Val Leu Lys Glu Glu Leu Ser			

225 230 235 240

Pro Ile Gln Pro Val Gly Lys Phe Leu Cys Val Lys Leu Val Val Phe

245 250 255

Val Ser Phe Trp

260

<210> 41

<211> 1918

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1082)..(1837)

<400> 41

ttattatgca gggtgttgat ttacataggg agttggagat gctaaccaag catggagttt 60

cacatgggtct atttctgctg agttcagggg cttggagaca gcctttaact tctggcaaaa 120

agacaatttc acaaaggtgt ttaaaaccat cctttgggtt ttgatcctga gtcagagacg 180

gacatgtgct tatgaaagaa ggtagagttt caacccttag gtaaccttaa aagagcagga 240

actatgttgt gtgtaagtca tgtgcagtat acaaacttga tattaaatga caaattggaa 300

caatctttct ctaggaatgc ctctctttca tagaggcatc acagtgagtc tcttaaagcc 360

ttgatctagg tgtgttacag atgggcttac agagtatgaa tgcacgataa gaaggaaatt 420

ggatagggag tgaggatatg aaatttaaaa gaaggaagaa gagaaaacga gattttaaga 480

caggaaatga agctctgtgt gtgtgtgtgt gtgtgtgtgc gcgtgtgtgt gtgcacgcgt 540

gcgtgcgtgt gtgcacgtgc gtgtgtgtgt gggtggcagg cctagtgatc ctgttgttta 600

gtgtctctga gatttgagtt gtgccttttt actttgcata aagtagatac ttggccatat 660

gtagttccaa ggagaagtca gagttccacc tttggagtct ttccttctga ttcacgattt 720

tctttcaaca attttccact taggaatcca tcacaaaagt tttgcacatg ctctacggaa 780

acttctgctg tgggcagtgt atcccactcg tcatctagag tctggtaaatt tgccaaagct 840

ggcagttgag actccttttag tttgaaaaat gatatcacct tcccattttc tttcatacca 900

ctgtccacca gaataaagag aatcttcccc tggaagagct tggctgcctt ctggtatctg 960

tgcattgttct ctccatactc tggggaggcc ttgttcatta tcaggaggag atgattctga 1020

attacgctgt tgaataaccc aatcacagtc acagggttgg agcaggagca ggagagggac 1080

a atg gaa gct gcc ccg tcc agg ttc atg ttc ctc tta ttt ctc ctc acg 1129

Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu Thr

1 5 10 15

tgt gag ctg gct gca gaa gtt gct gca gaa gtt gag aaa tcc tca gat 1177

Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser Ser Asp

20 25 30

ggc cct ggt gct gcc cag gaa ccc acg tgg ctc aca gat gtc cca gct 1225

Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp Val Pro Ala

35 40 45

gcc atg gaa ttc att gct gcc act gag gtg gct gtc ata ggc ttc ttc 1273

Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val Ile Gly Phe Phe

50 55 60

cag gat tta gaa ata cca gca gtg ccc ata ctc cat agc atg gtg caa 1321

Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu His Ser Met Val Gln

65 70 75 80

aaa ttc cca ggc gtg tca ttt ggg atc agc act gat tct gag gtt ctg 1369

Lys Phe Pro Gly Val Ser Phe Gly Ile Ser Thr Asp Ser Glu Val Leu

85 90 95

aca cac tac aac atc act ggg aac acc atc tgc ctc ttt cgc ctg gta 1417

Thr His Tyr Asn Ile Thr Gly Asn Thr Ile Cys Leu Phe Arg Leu Val

100 105 110

gac aat gaa caa ctg aat tta gag gac gaa gac att gaa agc att gat 1465

Asp Asn Glu Gln Leu Asn Leu Glu Asp Glu Asp Ile Glu Ser Ile Asp

115 120 125

gcc acc aaa ttg agc cgt ttc att gag atc aac agc ctc cac atg gtg 1513

Ala Thr Lys Leu Ser Arg Phe Ile Glu Ile Asn Ser Leu His Met Val

130 135 140

aca gag tac aac cct gtg act gtg att ggg tta ttc aac agc gta att 1561

Thr Glu Tyr Asn Pro Val Thr Val Ile Gly Leu Phe Asn Ser Val Ile

145 150 155 160

cag att cat ctc ctc ctg ata atg aac aag gcc tcc cca gag tat gaa 1609

Gln Ile His Leu Leu Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu

165

170

175

gag aac atg cac aga tac cag aag gca gcc aag ctc ttc cag ggg aag 1657

Glu Asn Met His Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys

180

185

190

att ctc ttt att ctg gtg gac agt ggt atg aaa gaa aat ggg aag gtg 1705

Ile Leu Phe Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val

195

200

205

ata tca ttt ttc aaa cta aag gag tct caa ctg cca gct ttg gca att 1753

Ile Ser Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile

210

215

220

tac cag act cta gat gac gag tgg gat aca ctg ccc aca gca gaa gtt 1801

Tyr Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val

225

230

235

240

tcc gta gag cat gtg caa aac ttt tgt gat gga ttc taagtggcaa 1847

Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe

245

250

attgttgaaa gaaaatcgtg aatcaggaag ggggaaaagg gactcccaaa aaggggttgg 1907

gggaaaaacc t

1918

<210> 42

<211> 252

<212> PRT

<213> Homo sapiens

<400> 42

Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu Thr

1 5 10 15

Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser Ser Asp

20 25 30

Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp Val Pro Ala

35 40 45

Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val Ile Gly Phe Phe

50 55 60

Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu His Ser Met Val Gln

65 70 75 80

Lys Phe Pro Gly Val Ser Phe Gly Ile Ser Thr Asp Ser Glu Val Leu

85

90

95

Thr His Tyr Asn Ile Thr Gly Asn Thr Ile Cys Leu Phe Arg Leu Val

100

105

110

Asp Asn Glu Gln Leu Asn Leu Glu Asp Glu Asp Ile Glu Ser Ile Asp

115

120

125

Ala Thr Lys Leu Ser Arg Phe Ile Glu Ile Asn Ser Leu His Met Val

130

135

140

Thr Glu Tyr Asn Pro Val Thr Val Ile Gly Leu Phe Asn Ser Val Ile

145

150

155

160

Gln Ile His Leu Leu Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu

165

170

175

Glu Asn Met His Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys

180

185

190

Ile Leu Phe Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val

195

200

205

175

Ile Ser Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile

210

215

220

Tyr Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val

225

230

235

240

Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe

245

250

<210> 43

<211> 1914

<212> DNA

<213> Homo sapiens

<220>

<223> The open reading frame was identified

beginning with an ATG initiation codon at nucleotides 1078-1080

and ending with a stop codon at nucleotides 1834-1836 on the

reverse complement of SEQ ID NO:43.

<400> 43

agggtttttcc cccaaccct ttttgggagt cccttttccc ccttctgat tcacgatttt 60

ctttcaacaa ttgccactt agaatccatc acaaaagttt tgcacatgct ctacggaaac 120

ttctgctgtg ggcagtgtat cccactcgtc atctagagtc tggtaaattg ccaaagctgg 180

cagttgagac tccttttagtt tgaaaaatga tatcaccttc ccattttctt tcataccact 240

gtccaccaga ataaagagaa tcttcccctg gaagagcttg gctgccttct ggtatctgtg 300

catgttctct tcatactctg gggaggcctt gttcattatc aggaggagat gaatctgaat 360

tacgctgttg aataacccaa tcacagtcac agggttgtac tctgtcacca tgtggaggct 420

gttgatctca atgaaacggc tcaatttggg ggcacaaatg ctttcaatgt cttcgtcctc 480

taaattcagt tggtcattgt ctaccaggcg aaagaggcag atgggtgtcc cagtgatgtt 540

gtagtgtgtc agaacctcag aatcagtgtc gatcccaaat gacacgctg ggaatttttg 600

caccatgcta tggagtatgg gcactgctgg tatttctaaa tcttgaaga agcctatgac 660

agccacctca gtggcagcaa tgaattccat ggcagctggg acatctgtga gccacgtggg 720

ttctgtggca gcaccaggac catctgagga tttctcaact tctgcagcaa cttctgcagc 780

cagctcacac gtgaggagaa ataagaggaa catgaacctg gacggggcag cttccattgt 840

ccctctcttg ctctgtctcc aaccctgtga ctgtgattgg gttattcaac agcgtaattc 900

agaatcatct cctcctgata atgaacaagg cctccccaga gtatggagag aacatgcaca 960

gataccagaa ggcagccaag ctcttcagg ggaagattct ctttattctg gtggacagtg 1020

gtatgaaaga aaatgggaag gtgatatcat tttcaaact aaaggagtct caactgccag 1080

ctttggcaat ttaccagact ctagatgacg agtgggatac actgcccaca gcagaagttt 1140

ccgtagagca tgtgcaaaac ttttgtgatg gattcctaag tggaaaattg ttgaaagaaa 1200

atcgtgaatc agaaggaaag actccaaagg tggaactctg acttctcctt ggaactacat 1260

atggccaagt atctacttta tgcaaagtaa aaaggcacia ctcaaattct agagacacta 1320

aacaacagga tcaactaggcc tgccaaccac acacacacgc acgtgcacac acgcacgcac 1380

gcgtgcacac acacacgcgc acacacacac acacacacag agcttcattt cctgtcttaa 1440

aatctcggtt tctcttcttc cttcttttaa atttcatatc ctcactccct atccaatttc 1500

cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga tcaaggcttt 1560

aagagactca ctgtgatgcc tctatgaaag agaggcattc ctagagaaag attgttccaa 1620

tttgtcattt aatatcaagt ttgtatactg cacatgactt acacacaaca tagttcctgc 1680

tcttttaagg ttacctaagg gttgaaactc taccttcttt cataagcaca tgtccgtctc 1740

tgactcagga tcaaaaacca aaggatggtt ttaaacacct ttgtgaaatt gtctttttgc 1800

cagaagttaa aggctgtctc caagtccttg aactcagcag aaatagacca tgtgaaactc 1860

catgcttggt tagcatctcc aactccctat gtaaatcaac aacctgcata ataa 1914

<210> 44

<211> 252

<212> PRT

<213> Homo sapiens

<400> 44

Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu Thr

1

5

10

15

Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser Ser Asp

20

25

30

Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp Val Pro Ala

35

40

45

Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val Ile Gly Phe Phe

50

55

60

Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu His Ser Met Val Gln

65

70

75

80

Lys Phe Pro Gly Val Ser Phe Gly Ile Ser Thr Asp Ser Glu Val Leu

85

90

95

Thr His Tyr Asn Ile Thr Gly Asn Thr Ile Cys Leu Phe Arg Leu Val

100

105

110

Asp Asn Glu Gln Leu Asn Leu Glu Asp Glu Asp Ile Glu Ser Ile Asp

115

120

125

Ala Thr Lys Leu Ser Arg Phe Ile Glu Ile Asn Ser Leu His Met Val

130

135

140

180

Thr Glu Tyr Asn Pro Val Thr Val Ile Gly Leu Phe Asn Ser Val Ile

145 150 155 160

Gln Ile His Leu Leu Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu

165 170 175

Glu Asn Met His Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys

180 185 190

Ile Leu Phe Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val

195 200 205

Ile Ser Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile

210 215 220

Tyr Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val

225 230 235 240

Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe

245 250

<210> 45

<211> 3082

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (460)..(2394)

<220>

<221> variation

<222> (1)..(3082)

<223> where n can be any nucleotide

<400> 45

gagctcggat ccactagtaa cggccgccag tgtgctggaa ttcggcttta cgactcacta 60

tagggctcga gcggctgccc gggcaggtca catttgtttg cctgattccc agctctctta 120

ggataggtct tcttgggaaa tgctttcatt tctaatacaa agaaaattgt gcaggcagcc 180

acgttaagat gtttttctga caataatcgg ccaagatatt ccactgtgtc tcgaggccac 240

tactgaaaag aggaagtttg ttttctgtt gttctgacag gaagaggtgg atctacttca 300

tcaacatgca gtaccaaatt gttaggatac aagctaaaaa ggaggggtggt tttttccact 360

ttgttgaatt gttcctatac tcaaaattgc accaagacac cttgtctccc aaatgcaaaa 420

tgtgaaatac gcaatggaat tgaagcctgc tattgcaac atg gga ttt tca gga 474

Met Gly Phe Ser Gly

1 5

aat ggt gtc aca att tgt gaa gat gat aat gaa tgt gga aat tta act 522

Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn Leu Thr

10 15 20

cag tcc tgt ggc gaa aat gct aat tgc act aac aca gaa gga agt tat 570

Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly Ser Tyr

25 30 35

tat tgt atg tgt gta cct ggc ttc aga tcc agc agt aac caa gac agg 618

Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln Asp Arg

40 45 50

ttt atc act aat gat gga acc gtc tgt ata gaa aat gtg aat gca aac 666

Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn Ala Asn

55 60 65

tgc cat tta gat aat gtc tgt ata gct gca aat att aat aaa act tta 714

Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys Thr Leu

70

75

80

85

aca aaa atc aga tcc ata aaa gaa cct gtg gct ttg cta caa gaa gtc 762

Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln Glu Val

90

95

100

tat aga aat tct gtg aca gat ctt tca cca aca gat ata att gca tat 810

Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile Ala Tyr

105

110

115

ata gaa ata tta gct gaa tca tct tca tta cta ggt tac aag aac aac 858

Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys Asn Asn

120

125

130

act atc tca gcc aag gac acc ctt tct aac tca act ctt act gaa ttt 906

Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr Glu Phe

135

140

145

gta aaa acc gtg aat aat ttt gtt caa agg gat aca ttt gta gtt tgg 954

Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val Val Trp

150

155

160

165

gac aag tta tct gtg aat cat agg aga aca cat ctt aca aaa ctc atg 1002

Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys Leu Met

170

175

180

cac act gtt gaa caa gct act tta agg ata tcc cag agc ttc caa aag 1050

His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe Gln Lys

185

190

195

acc aca gag ttt gat aca aat tca acg gat ata gct ctc aaa gtt ttc 1098

Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys Val Phe

200

205

210

ttt ttt gat tca tat aac atg aaa cat att cat cct cat atg aat atg 1146

Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met Asn Met

215

220

225

gat gga gac tac ata aat ata ttt cca aag aga aaa gct gca tat gat 1194

Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala Tyr Asp

230

235

240

245

tca aat ggc aat gtt gca gtt gca ttt gta tat tat aag agt att ggt 1242

Ser Asn Gly Asn Val Ala Val Ala Phe Val Tyr Tyr Lys Ser Ile Gly

250

255

260

cct ttg ctt tca tca tct gac aac ttc tta ttg aaa cct caa aat tat 1290

Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln Asn Tyr

265

270

275

gat aat tct gaa gag gag gaa aga gtc ata tct tca gta att tca gtc 1338

Asp Asn Ser Glu Glu Glu Glu Arg Val Ile Ser Ser Val Ile Ser Val

280

285

290

tca atg agc tca aac cca ccc aca tta tat gaa ctt gaa aaa ata aca 1386

Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys Ile Thr

295

300

305

ttt aca tta agt cat cga aag gtc aca gat agg tat agg agt cta tgt 1434

Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser Leu Cys

310

315

320

325

gca ttt tgg aat tac tca cct gat acc atg aat ggc agc tgg tct tca 1482

Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp Ser Ser

330

335

340

gag ggc tgt gag ctg aca tac tca aat gag acc cac acc tca tgc cgc 1530

Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser Cys Arg

345

350

355

tgt aat cac ctg aca cat ttt gca att ttg atg tcc tct ggt cct tcc 1578

Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly Pro Ser

360

365

370

att ggt att aaa gat tat aat att ctt aca agg atc act caa cta gga 1626

Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln Leu Gly

375

380

385

ata att att tca ctg att tgt ctt gcc ata tgc att ttt acc ttc tgg 1674

Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr Phe Trp

390

395

400

405

ttc ttc agt gaa att caa agc acc agg aca aca att cac aaa aat ctt 1722

Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys Asn Leu

410

415

420

tgc tgt agc cta ttt ctt gct gaa ctt gtt ttt ctt gtt ggg atc aat 1770

Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly Ile Asn

425

430

435

aca aat act aat aag ctc ttc tgt tca atc att gcc gga ctg cta cac 1818

Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu Leu His

440

445

450

tac ttc ttt tta gct gct ttt gca tgg atg tgc att gaa ggc ata cat 1866

Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly Ile His

455

460

465

ctc tat ctc att gtt gtg ggt gtc atc tac aac aag gga ttt ttg cac 1914

Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe Leu His

470

475

480

485

aag aat ttt tat atc ttt ggc tat cta agc cca gcc gtg gta gtt gga 1962

Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val Val Gly

490

495

500

ttt tcg gca gca cta gga tac aga tat tat ggc aca acc aaa gta tgt 2010

Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys Val Cys

505

510

515

tgg ctt agc acc gaa aac aac ttt att tgg agt ttt ata gga cca gca 2058

Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly Pro Ala

520

525

530

tgc cta atc att ctt gtt aat ctc ttg gct ttt gga gtc atc ata tac 2106

Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile Ile Tyr

535

540

545

aaa gtt ttt cgt cac act gca ggg ttg aaa cca gaa gtt agt tgc ttt 2154

Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser Cys Phe

550 555 560 565

gag aac ata agg tct tgt gca aga gga gcc ctc gct ctt ctg ttc ctt 2202

Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu Phe Leu

570 575 580

ctc ggc acc acc tgg atc ttt ggg gtt ctc cat gtt gtg cac gca tca 2250

Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His Ala Ser

585 590 595

gtg gtt aca gct tac ctc ttc aca gtc agc aat gct ttc cag ggg atg 2298

Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln Gly Met

600 605 610

ttc att ttt tta ttc ctg tgt gtt tta tct aga aag att caa gaa gaa 2346

Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln Glu Glu

615 620 625

tat tac aga ttg ttc aaa aat gtc ccc tgt tgt ttt gga tgt tta agg 2394

Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys Leu Arg

630 635 640 645

taaacataga gaatggtgga taattacaac tgcacaaaaa taaaaattcc aagctgtgga 2454

tgaccaatgt ataaaaatga ctcacaaat tatccaatta ttaactacta gacaaaaagt 2514

attttaaatc agtttttctg tttatgctat aggaactgta gataataagg taaaattatg 2574

tatcatatag atatactatg tttttctatg tgaaatagtt ctgtcaaaaa tagtattgca 2634

gatatttgga aagtaattgg tttctcagga gtgatatcac tgcaccaag gaaagatttt 2694

ctttctaaca cgagaagtat atgaatgtcc tgaaggaaac cactggcttg atatttctgt 2754

gactcgtggt gcctttgaaa ctagtcccct accacctcgg taatgagctc cattacagaa 2814

agtggaacat aagagaatga aggggcagaa tatcaaacag tgaaaaggga atgataagat 2874

gtattttgaa tgaactgttt tttctgtaga ctagctgaga aattgttgac ataaaataaa 2934

gaattgaaga aacacatttt accattttgt gaattgttct gaacttaaata gtccactaaa 2994

acaacttaga cttctgtttg ctaaactctgt ttctttttct aatattctaa aaaaaaaaaa 3054

aaggtttacc tccacaaatt gaaaaaan 3082

<210> 46

<211> 645

<212> PRT

<213> Homo sapiens

<400> 46

Met Gly Phe Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu

1 5 10 15

Cys Gly Asn Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn

20 25 30

Thr Glu Gly Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser

35 40 45

Ser Asn Gln Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu

50 55 60

Asn Val Asn Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn

65 70 75 80

Ile Asn Lys Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala

85 90 95

Leu Leu Gln Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr

100

105

110

Asp Ile Ile Ala Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu

115

120

125

Gly Tyr Lys Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser

130

135

140

Thr Leu Thr Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp

145

150

155

160

Thr Phe Val Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His

165

170

175

Leu Thr Lys Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser

180

185

190

Gln Ser Phe Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile

195

200

205

Ala Leu Lys Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His

210

215

220

Pro His Met Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg

225 230 235 240

Lys Ala Ala Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Val Tyr

245 250 255

Tyr Lys Ser Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu

260 265 270

Lys Pro Gln Asn Tyr Asp Asn Ser Glu Glu Glu Glu Arg Val Ile Ser

275 280 285

Ser Val Ile Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu

290 295 300

Leu Glu Lys Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg

305 310 315 320

Tyr Arg Ser Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn

325 330 335

Gly Ser Trp Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr

340 345 350

His Thr Ser Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met

355

360

365

Ser Ser Gly Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg

370

375

380

Ile Thr Gln Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys

385

390

395

400

Ile Phe Thr Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr

405

410

415

Ile His Lys Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe

420

425

430

Leu Val Gly Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile

435

440

445

Ala Gly Leu Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys

450

455

460

Ile Glu Gly Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn

465

470

475

480

Lys Gly Phe Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro

485

490

495

Ala Val Val Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly

500

505

510

Thr Thr Lys Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser

515

520

525

Phe Ile Gly Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe

530

535

540

Gly Val Ile Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro

545

550

555

560

Glu Val Ser Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu

565

570

575

Ala Leu Leu Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His

580

585

590

Val Val His Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn

595

600

605

Ala Phe Gln Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg

610

615

620

Lys Ile Gln Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys

625

630

635

640

Phe Gly Cys Leu Arg

645

<210> 47

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically

synthesized

<400> 47

aaaaaggagg agtcaaacgt gtct

24

<210> 48

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 48

ggccaagcgc agctttgc

18

<210> 49

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 49

cccatcgacc acatcctcct ccag

24

<210> 50

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 50

taaagagaat cttcccctgg aagag

25

<210> 51

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 51

ggcctcccca gagtatgga

19

<210> 52

<211> 27

<212> DNA

<213> Homo sapiens

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 52

catgcacaga taccagaagg cagccaa

27

<210> 53

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically

synthesized

<400> 53

ggatgcatgc tccaaagaag a

21

<210> 54

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically

synthesized

<400> 54

ctcaccact gctgtctcca

20

<210> 55

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 55

ctgcccaggt ggccgtcact c

21

<210> 56

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 56

gctccccaat ctggtctect ac

22

<210> 57

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 57

gatgggcttg aactggaaag ag

22

<210> 58

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 58

ctctctgtgt gccacccatg ctgg

24

<210> 59

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 59

cgcacagtca catggtcga

19

<210> 60

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 60

cagggcgacg ttgtgacag

19

<210> 61

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 61

tagtttccga agccccagta tcccacc

27

<210> 62

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 62

gaacgccgga gcatacaga

19

<210> 63

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 63

gatgccacag gccaca

17

<210> 64

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 64

ccagggtactg cacaacacg gcttcat

27

<210> 65

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 65

ccagggtactg cacaacacg gcttcat

27

<210> 66

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 66

ctgggacatt tttctgagcc tt

22

<210> 67

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 67

ccctggcacc gtgtccgctt

20

<210> 68

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 68

aaatcgcaag acattcactg tca

23

<210> 69

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 69

ccgccactcc atcatcact

19

<210> 70

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 70

cagcacactg gacttccgag tggacc

26

<210> 71

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 71

gcagtacaac cgggtagatg c

21

<210> 72

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 72

gcctctcagg gtgctattgg

20

<210> 73

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 73

gcctctcagg gtgctattgg

20

<210> 74

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 74

ggtaggtcgac ttaatggtga tggatgatgat ggtggctcgg ggatgtttcc ccggtt 55

<210> 75

<211> 305

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (303)

<400> 75

atg cca cat ctg tat ata gat ggg gtt ttt cca ata cag ctg gtt cgt 48

Met Pro His Leu Tyr Ile Asp Gly Val Phe Pro Ile Gln Leu Val Arg

1 5 10 15

gat aaa ctg cat gaa act cct gcc gtc ctg cgc ctg ctg ggg cct cca 96

Asp Lys Leu His Glu Thr Pro Ala Val Leu Arg Leu Leu Gly Pro Pro

20 25 30

ggc aag gcc acg tgg ggt tgg ggg tgg ggc tgg tcc ttc tcc ctc ccc 144

Gly Lys Ala Thr Trp Gly Trp Gly Trp Gly Trp Ser Phe Ser Leu Pro

35 40 45

agg cct gtg ttc ttg ggg ctg ctc cca tgc aga cag gat cac cta aca 192

Arg Pro Val Phe Leu Gly Leu Leu Pro Cys Arg Gln Asp His Leu Thr

50 55 60

gag atg gaa gcc agg gca tgg atg ggg ctt tgg gtc ctc gag gtt gga 240

Glu Met Glu Ala Arg Ala Trp Met Gly Leu Trp Val Leu Glu Val Gly

65 70 75 80

ccc cag ctt ctt gcc acc ttc ccc tcc ggg cag tca gct ctc cat cca 288

Pro Gln Leu Leu Ala Thr Phe Pro Ser Gly Gln Ser Ala Leu His Pro

85 90 95

tcc ccc tct tta atc ta

305

Ser Pro Ser Leu Ile

100

<210> 76

<211> 101

<212> PRT

<213> Homo sapiens

<400> 76

Met Pro His Leu Tyr Ile Asp Gly Val Phe Pro Ile Gln Leu Val Arg

1

5

10

15

Asp Lys Leu His Glu Thr Pro Ala Val Leu Arg Leu Leu Gly Pro Pro

20

25

30

Gly Lys Ala Thr Trp Gly Trp Gly Trp Gly Trp Ser Phe Ser Leu Pro

35

40

45

Arg Pro Val Phe Leu Gly Leu Leu Pro Cys Arg Gln Asp His Leu Thr

50

55

60

Glu Met Glu Ala Arg Ala Trp Met Gly Leu Trp Val Leu Glu Val Gly

65

70

75

80

Pro Gln Leu Leu Ala Thr Phe Pro Ser Gly Gln Ser Ala Leu His Pro

85

90

95

Ser Pro Ser Leu Ile

100

<210> 77

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically

synthesized

<400> 77

ggatccgaag ttgagaaatc ctcagatggt

30

<210> 78

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 78

ctcgagaggg ttgtactctg tcaccatgtg

30

<210> 79

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 79

ggatccacca tgcggacact cttcaacctc ctctgg

36

<210> 80

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 80

ctcgaggagc aggtcgtaga agtagtccag g

31

<210> 81

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 81

cgtcggatcc tatgtcaagt gccgtctcaa cgtgctgctc tggtag

46

<210> 82

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 82

cgtcctcgag ttaatggtga tggatgatgat gcatatcatc cttggacacc aggcag 56

<210> 83

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 83

ggatccaaga ataaagttaa aggcagc

27

<210> 84

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 84

gtcgacgcca gccaaagcat taggatcatg cac

33

<210> 85

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 85

cgggatccac catgtcaagc cctgcttcca cctgcatag

39

<210> 86

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 86

cgctcgagac tgaatggata catgaaaaga aaggaacaaa gaggtg

46

<210> 87

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 87

ccgctcgagt gagcccaaattttgtgacaa a

31

<210> 88

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 88

gctctagact tttacccggg gacagggag

29

<210> 89

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 89

aattctgcag cgaaaacctg tattttcagg gt

32

<210> 90

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 90

tcgaaccctg aaaatacagg ttttcgctgc ag

32

<210> 91

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 91

ctcgtcctcg agggtaagcc tatccctaac

30

<210> 92

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 92

ctcgtcgggc ccctgatcag cgggtttaa c

31

<210> 93

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chemically
synthesized

<400> 93

cgtcggatcc atgccacatc tgtatataga tggggttttt cc

42